Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 192, Appli Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 1250, Appl Sequence 1250, Appli Sequence 1250, Appli Sequence 1250, Appli Sequence 1250, Appli Sequence 113, Appli Sequence 113, Appli Sequence 7, Appli

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GENERAL INFORMATION:
APPLICANT: COCKS, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: COMPOSITION FOR THE DETECTION OF
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1144 PORTER BRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER: IBAP CCOMPALIBLE
COMPUTER: IBAP CCOMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MOOF PERFECT 6.1 for Windows/MS-DOS SOFTWARE: MOOF PERFECT 6.1 for Windows/MS-DOS SOFTWARE: HEREWITH
CLASSIFICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
FRING APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTACL
                                     US-08-916-421B-13
US-08-916-421B-13
US-08-918-322-1423
US-08-918-322-1423
US-08-459-831-3
US-09-453-702B-192
US-09-453-702B-192
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US-09-453-702B-192
US-08-458-831-19
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US-09-252-991A-1329
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US-08-91S-337-1
US-08-91S-337-1
US-08-91S-337-1
US-08-91S-337-1
US-08-461-146C-7
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CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
MAME: Zeller, Karen J.
REGISTRATION WUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-023-655-79
Sequence 79, Application US/09023655
Sequence No. 6607879
Patent No. 6607879
GENERAL INFORMATION
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Sequence 26, Appl
Sequence 1774, Appl
Sequence 12137, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 8, Appli
                                                                                                                                                                                      March 17, 2004, 16:42:09 ; Search time 69 Seconds (without alignments) 651.464 Million cell updates/sec
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Sequence 2
Sequence 3
                                                                                                                                                                                                                                                                                             US-09-648-310-4
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2. (cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4. /cgn2_6/ptodata/2/ina/RB_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6. /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-644-460-26
US-09-228-352-1774
US-08-252-991A-12137
US-08-358-901-1
US-08-566-347-1
US-08-663-347-1
US-08-656-347-1
US-08-656-347-1
US-08-656-347-1
US-08-128-18
US-09-138-97A-8
US-09-138-97A-8
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US-09-138-000C-2571
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Maximum Match 100%
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Match Length DB
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Ygapop 10.0
Fgapop 6.0
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fect score:
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THE DETECTION OF BLOOD CELL GENE

Sequence 9, P Sequence 9, P Sequence 9, P Sequence 9, P Sequence 13,

Percent Simil Best Local Si Query Match: DB:	US-09-648-310	ç	Db 170	Oy 21	Db 23(	Qy 4.	Db 29(	6y 60	35.	Qy 8	Db 41	RESULT 3 US-09-328-35; Sequence 1	<pre>; Patent No. ; GENERAL IN ; APPLICANT</pre>	; TITLE OF	FILE REFE CURRENT A	SEQ ID NO LENGTH:	) ORGANISM US-09-328-35	Alignment So Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	US-09-648-31	ò	Db 139	. Yo	Db 145	δy	Db 151	δy	15.	RESULT 4 US-09-252-99	
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E: (6 (650 FOR SE HARACT	LENGTH: 786 base pairs TYPE: nucleic acid	ESS: lin	IMMEDIATE SOURCE: LIBRARY: THP1PLB01	CLONE: 012364 -09-023-655-79	:	4.35e-50 Length: 371.00 Matches:	larity: 96.43% imilarity: 96.43%	Indels: Gaps:	3-09-648-310-4 (1-81) x US-09-023-655-79 (1-786)	1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20	140 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 199	21 ASRAlaASpGlyLysLeuSer-Vallys-PheGlyValLeuPheArgAspLysCysA 40	. 40 laAsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAla-LysArgArgLysIleVal 59	260 CCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAAAGGAAGG	60 ThrTyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAsplelleleuLeu 79	GlnAsp	380 CAAGAI 385 SIII.T 2	S-09-644-460-26 Sequence 26, Application US/09644460 Sequence 26, Application US/09644460 Sequence 26, Application US/09644460 Sequence 26, Application US/09644460 GENERAL INFORMATION: APPLICANT: Fisher, Paul B. TITLE OF INVENTION: Reciprocal Subtraction Differential TITLE OF INVENTION: Display FILE REFERENCE: 34587-C-PCT-USA	CURRENT APPLICATION NUMBER: US/09/644,460 CURRENT FILING DATE: 2000-08-23	PRIOR APPLICATION NUMBER: PCT/US99/04323 PRIOR FILING DATE: 1999-02-26	PRIOR APPLICATION NUMBER: US 09/197,889 PRIOR FILING DATE: 1998-11-23	PRICR APPLICATION NUMBER: US 09/185,115 PRICR FILING DATE: 1998-11-03	PRIOR APPLICATION NUMBER: US 09/032,684 PRIOR FILING DATE: 1998-02-27	NUMBER OF SEQ ID NOS: 42 SOFTWARE: FastSEQ for Windows Version 4.0	SEQ ID NO 26 LENGTH: 800	ORGANISM: h	15-09-644-460-20	11.gnment Scores: 5.06e-47 Length: 800 Yred. No.: 352.00 Matches: 74	

			BACTER		
rity: 93.98% Conservative: 4 ilarity: 89.16% Mismatches: 3 Indels: 2 4 Gaps: 0	4 (1-81) x US-09-644-460-26 (1-800)  MetabnvalaspHisGluValAsmLeuteuValGluGluIleHisArgLeuGlySerLys 20  ArgaAcGrGGAGGATGAGGTTAACCTCCTGGTGGAGGAATTCATCGTCTGGGTTCCAAA 229  ASDALAASPGLYVSLEUSErValLySPheGlyValLeuPheArgAspAspLysCysAla 40  ASTACGATGGGAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACGAGTGCC 289  AsnLeuPheGluAla-LeuValGlyThrLeuLyShla-AlaLySArgArgLysIleValT 60	hrtyrProGlyGluLeuLeuLeuGhnGlyValHisAspAspValAsplleIleLeuLeuG 80	RESULT 3  US-09-328-352-1774  Sequence 1774, Application US/09328352  Patent NO. 6562958  GENERAL INFORMATION: TITLE OF INVENTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: WICHEL US/09/328,352  CURRENT APPLICATION NUMBER: US/09/328,352  CURRENT FILING DATE: 1999-06-04  NUMBER OF SEQ ID NOS: 8252  IENGTH: 2133  TYPE: DN  CRACALISM: Acinetobacter baumannii US-09-328-352-1774	1.95 Length: 66.0 Matches: 50.67% Conservativ y: 32.00% Mismatches: 16.10% Gaps:	10-4 (1-81) x US-09-328-352-1774 (1-2133)  1 MetAsnValAspHisGluValAsnLeuLeuValGluIleHisArgLeuGlySerLys 20  1 H
nnt Similarity: Local Similarity Match:	1 170 21 230 230 290	60 350 80 410	ILT 3 19-328-352. 49-328-352. AUGUENCE 17. INTER OF III TILE REFERENT PITTLE OF III TILE REFERENT APPLIANSENT APPL	ent Sc No.: t Simi ccal S	-09-648-310 1396 21 1453 37 1513 1513 1573 1574
Percent Best Lo Query M	40 40 40 40 40 40	6666	RESULT US-09-1 Sacque RESULT GENE TIT TIT TIT TIT TIT TIT SED	Alignm Pred. Score: Percen Best Duery DB:	US-0 OY OY OY OY OY OY OY OY OY OY OY

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1029 Grechegegecringgeadagagecriceaacaccingaaagcricerreaarcriceag 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 HisGluValAsnLeuleuValGluGluIleHisArgLeuGlySerLysAsnAlaAspGly
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Patent No. 5633450

GENERAL INFORMATION:
APPLICANT: Sualow, Trevor V,
APPLICANT: Jones, Jonathan D.G,
TITLE OF INVENTION: No. 5633450el Chitinase-Producing Plants
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCES ADDRESS: 1
CORRESPONDENCE ADDRESS: 1
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
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                FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/550,253

FILING DATE: 09-JUL-1990

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 18-JUL-1986

PRIOR APPLICATION DATA: US 06/593,691

FILING DATE: 26-MAR-1984

ATTORNEY/AGENT INFORMATION:
NAME: SMITH, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/OOCKET NUMBER: 12176-5-3

TELECHONICATION INFORMATION:
TELEPHONE: 415-326-2400

TELEPHONE: 
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MOLECULE TYPE: DNA (genomic)
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29.41%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
361..2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-08-566-347-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY:
, LOCATION:
US-08-358-901-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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equence 12137, Application US/09252991A

atent No. 6551795

ENERAL INFORMATION:
APPLICAMT:
APPLICAMT:
MAIC J. Rubenfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
APPLICATION WINBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

EQ ID NO 12137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 GACATCGCCCCCCAGCTCGCGGCGGTGAAGCGCGGTGACGGCCGCAAAGCGCGTTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 cacaccaracercarcricaccacarcaradagargarcanagacanarcriator 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AsnalaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1. Application US/08358901
Satent No. 5554521
GENERAL INFORMATION:
APPLICANT: Suslow, Trevor V.
APPLICANT: Once, Jonathan D.G.
TITLE OF INVENTION: No. 5554521e1 Chitinase-Producing Plants
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-648-310-4 (1-81) x US-09-252-991A-12137 (1-393)
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
09-252-991A-12137
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64.50
39.51%
25.93%
15.73%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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t Local Similarity:
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d. No .
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
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|CTGTCGTTGATGCCATTGCCGCCGCAGATCGGGATAAAGCCGTACAGCAGGTGGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 HisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLysAsnAlaAspGly 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 LysieuSerValLysPheGlyValLeuPheArgAspAspLysCysAlaAsnLeuPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Suelow, Trevor V.
APPLICANT: Jones, Jonathan D.G.
TITLE OF INVENTION: No. 5776448el Chitinase-Producing Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2323
20
16
31
             COMPUTER: IEM PC Compatible
COMPATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,347
FILING DATE: U-DEC-1995
CLASSIFICATION NUMBER: US/08/56,901
FILING DATE: 19-DEC-1994
PROOR APPLICATION NUMBER: US/08/58,901
FILING DATE: 19-DEC-1994
PROOR APPLICATION NUMBER: US/05/0,253
FILING DATE: 09-UUL-1990
PROOR APPLICATION DATA:
APPLICATION NUMBER: US/06/888,033
FILING DATE: 18-UUL-1986
PRILING DATE: 26-MR-1984
ATTONEY/AGANTION NUMBER: US/06/593,691
FILING DATE: 26-MR-1984
ATTONEY/AGANTIN NUMBER: US/06/593,691
FILING DATE: 26-MR-1084
ATTONEY/AGANTINN INFORMATION:
TELEEPHONE: ATS-26-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent No. 5776448
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2323 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.50
52.94%
29.41%
15.73%
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sst Local Similarity:
lery Match:
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LOCATION:
3-08-566-347-1
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1086 CACGCCTTCTGCGCCTTTTGCAGCGCGGAACGGATCGTGGATCGAGATTTTGAA--- 1030
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                                                                                                      SIREALI AND CONTEXT.

CITY: California
CONTRY: USA
ZIPI: 94111-3834

ZURE: California
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPAS.
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/693,835
FILING DATE: 101-AUG-1996
CLASSIFICATION NUMBER: US 06/358,901
FILING DATE: 19-DEC-1994
PRIOR APPLICATION NUMBER: US 06/898,033
FILING DATE: 19-DEC-1994
PRIOR APPLICATION NUMBER: US 06/898,033
FILING DATE: 18-ULJ-1986
PRIOR APPLICATION NUMBER: US 06/593,691
FILING DATE: 26-DAR-1984
ATTORNEY/AGENT INFORMATION:
FELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
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Mismatches:
Indels:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.50
52.94%
29.41%
15.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 361..2043
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906 TIGCGCCGGGATCTIGTCGAC 886
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 1..2329
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 LeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGluLeu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 LeuSerValLysPheGlyValLeuPheArgAspAspLysCysAlaAsnLeuPheGluAla 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

LOCATION: 1..2329

IDENTIFICATION METHOD: experimental
OTHER INPORMATION: /function= "exo-chitinase"
OTHER INPORMATION: /product= "Chis protein"
OTHER INFORMATION: /evidence= Experimental
OTHER INFORMATION: /cvidence= Experimental
OTHER INFORMATION: /cvidence= leaquence listing of the Chis gene from oTHER INFORMATION: plasmid plchis from E.coli A 5187"
                                                                                                                                                                                                                                   Transgenic pathogen-resistant organism 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,797A
FILING DATE: Unne 1, 1995
ATTORNEY FAGENT INPREMATION:
REGISTRATION NUMBER: 18,839
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
TELECOMMUNICATION INPREMATION:
              SULT 8
-08-457-797A-8/c
Sequence 8, Application US/08457797A
Sequence 8, Application US/08457797A
Patent NO. 5689045
GENERAL INFORMATION:
APPLICANT:
ATITUE OF INVENTION: Transgenic pathogen-resistant organi
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
CITY: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-09-648-310-4 (1-81) x US-08-457-797A-8 (1-2329)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNMEDIATE SOURCE: | TERMEDIATE SOURCE: | TERMEDIATE |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 238555
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2329 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.00
55.32%
36.17%
15.61%
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3: CDNA
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sst Local Similarity:
lery Match:
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MOLECULE TYPE: c
ORIGINAL SOURCE:
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1026 croscosocoradodadoscridonacidocoradanacoracoracidaricaria 267
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LeuServalLysPheGlyvalLeuPheArgAspAspLysCysAlaAsnLeuPheGluAla
US-08-812-025-8/C

1US-08-812-025-8/C

Sequence 08, Application US/08812025

Patent No. 5804184

GENERAL INPORMATION:

TITLE OF INVENTION: Transgenic pathogen-resistant organism
TITLE OF INVENTION: Transgenic pathogen-resistant organism
TUTLE OF INVENTION: Transgenic pathogen-resistant organism
NUMBER OF SEQUENCES:

ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond
STREET: 30 Rockefeller Plaza
CITY: New York
COMPTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Elopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/08/912,025

FILING DATE:
REGISTRATION NUMBER: 35,225

TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1NPORMATION:
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Mismatches:
Indels:
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ORIGINAL SOURCE:
ORGANISM: Serratia marcescens
IMMEDIATE SOURCE:
LIBRARY: Cosmid bank from Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-648-310-4 (1-81) x US-08-812-025-8 (1-2329)
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Matches:
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NAME/KEY: misc_feature
LOCATION: 1.2329
LOCATION: 1.2329
LOCATICON WETHOD: experimental
OTHER INFORMATION: /function= "exo-chitinase"
OTHER INFORMATION: /function= "Edis procein"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /nore= "sequence listing of the Chis gene from a OTHER INFORMATION: /nore= "sequence listing of the Chis gene from a OTHER INFORMATION: plasmid plChis from E.coli A 5187"
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Transgenic pathogen-resistant organism NUMBER OF SEQUENCES: 12
CADRESPONDENCE ADDRESS:
ADDRESSE: Baker & Botts
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READSLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cosmid bank from Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/138,873A FILING DATE: August 24, 1998 ATTORNEY/AGENT INFORMATION;
                                                                                                      906 TIGCGCCGGGATCTIGICGAC 886
                                                                     66 LeuLeuGlnGlyValHisAsp 72
                                                                                                                                                                                      5-09-138-873A-8/c
Sequence 8, Application US/09138873A
Patent No. 6271438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: Cosmid to PRARTIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Tenser, Arthur
REGISTRATION NUMBER: 19,839
NAME: KOIG, Lisa
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A2954
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 238555
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH 2329 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lignment Scores:
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26 LeuSerValLysPheGlyValLeuPheArgAspAspLysCysAlaAsnLeuPheGluAla 45

Indels:

64.00 55.32% 36.17% 15.61%

Percent Similarity: Sest Local Similarity: Query Match:

core:

IS-09-648-310-4 (1-81) x US-09-138-873A-8 (1-2329)

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GENERAL INFORMATION:
APPLICANT: Shylan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 0734-07401
CURRENT APPLICATION NUMBER: 1998-12-23
CURRENT FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2571, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PELING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 6812
SOOTWARE: Patentin Version 3.1
SEQ ID NO 2551
1026 CICGCGGCCCTGGCAGAGAGCGCAGAAGCTGCCTTCAATCTCTTTCAGGCT 967
                                                                                                                                                           966 Gregificarecearrecedecedearecedearaaagecedracageredegeregerr 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 CCTGCAGGAGGGATGACACGCTTACTTTATACAGATTCGTGGTTGGCAGCACAAAGTAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 GTGCAAAGCCAAACTGAGGGGTTTTGGACTGGAAACGCAATTTGACGAAGTCGGGAATCTG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GAATTTĊĊT 264
                                                                                             46 LeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThrTyrProGlyGluLeu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AsnAlaAspGlyLysLeuSerVal------ 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-648-310-4 (1-81) x US-09-134-000C-2571 (1-1278)
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Matches:
                                                                                                                                                                                                                                                                  906 TTGCGCCGGGATCTTGTCGAC 886
                                                                                                                                                                                                                            66 LeuleuGlnGlyValHisAsp 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000C-2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-134-000C-2571
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US-09-220-132-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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us-09-648-310-4.p2n.rni

Oy 5 HisGluvalAsnLeuLeuValGlubb 593 CACAGCATCAGCCTGGCGGCGAA  Oy 16	473 AAACTCACCGATTCCGGGGGTT 46 LeuValGlyThrLeuLySAla 116 CTGCGTGGCGTCTGTGCCGAG 61 TyrProGlyGluLeuLeu 66	DD 356 GTACCCGGCAGCCIGCTG 339 RESULT 14 US-00-252-991A-5307 Sequence 5307, Application US/09252 Petent No. 6551795	INFORMATION: ANT: MACC J. DF INVENTION: DF INVENTION: EFFRENCE: 107 E PELLICATION NUMBER APPLICATION NUMBER APPLICATION NUMBER APPLICATION NUMBER  APPLICATION NUMBER	HILLOW FALLOW DATE: 1998-06-18 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27 PRIOR SEQ ID NOS: 33142 EBNGTH: 954 PYPE: DNA CRANISM: Pseudomonas aeruginosa US-09-282-991A-5307	Alignment Scores:  Pred. No.:  Score:  Score:  Score:  Percent Similarity:  15.24  DB:  US-09-648-310-4 (1-81) × US-09-252-99  Qy  FlisGluValAshLeuLeuValGl  Db  127 CACAGCATCAGCGCCGAGGCCGAC  Oy  16
PRIOR APPLICATION NUMBER: US 60/079,303 PRIOR FILING DATE: 1998-03-25 PRIOR FILING DATE: 1998-12-24 NUMBER OF SEQ ID NOS: 191 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 30 LENGTH: 14770 TYPE: DNA ORGANISM: Homo sapiens	gnment Scores: 97.3 Length: 14770 xc. No.: 63.00 Marches: 27 xcent Similarity: 40.43\$ Conservative: 11 xt Local Similarity: 28.72\$ Mismatches: 26 xry Match: 15.37\$ Gaps: 4	.09-648-310-4 (1-81) x US-09-220-132-30 (1-14770) 6 GluValAsmieuleuValGluGluIleHisArgleuGlySeriysAsmAlaAspGlyLys 25	26 LeuServalLysPheGlyValLeuPheArgAspAspLysCysAlaAsn 41	62 ProGlyGluLeuLeuGlnGly	SULT 13 SQUET 13 SQUET 13 SQUED 19-22-991A-5194/C SQUENCE 5194, Application US/0925291A SQUENCE 5194, Application US/0925291A SQUENCE 5195 SEQUENCE 5195 SEQUENCE 10 FORWARTION: APPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: MOLDEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136 CURRENT FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 5:94 LENGTH: 675 TYPE: DNA ORGANISM: Pseudomonas aeruginosa O9-252-991A-5194 ignment Scores: Conservative: 9 Indels: 25 Indels: 35 CCCC 15 Indels: 35 CCCC 252-991A-5194 Indels: 35 CCCC 350 CCCC 3

9 HactuvalAenteuleuvaigningille
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SULT 15
-08-916-421B-1/c
Sequence 1. Application US/08916421B
Parent No. 6503729
GENERAL INFORMATION:
PAPLICANTE BUIL et al.
TITLE OF INVENTION:
Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITLE OF INVENTION: Jannaschii
FILLE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
FILLE REFERENCE: PB275
CURRENT FILLNG DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
PRIOR PAPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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LOCATION: (2822). (28222)

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CHER INFORMATION: n equals a, t, c, or g

LOCATION: (28257). (28258)

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NAME/KEY: misc_feature

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OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

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LOCATION: (39120). (98159)

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NAME/KEY: misc_feature

LOCATION: (39120). (98123)

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LOCATION: (3926). (98239)

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LOCATION: (3926). (19398)

OTHER INFORMATION: n equals a, t, c, or g

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LOCATION: (39243). (19398)

OTHER INFORMATION: n equals a, t, c, or g

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LOCATION: (39243). (19398)

OTHER INFORMATION: n equals a, t, c, or g

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LOCATION: (103989). (103989)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (103989). (103989)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (103989). (19398)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

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NAME/KEY: misc_feature
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LOCATION: (74364)...(64435)

OTHER INFORMATION: n equals a, t, c, or g
NAME/EXP: misc\_feature
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                                                                                                                                                                                                                                   52 AlaAlaLygArgArgLyg------!leValThrTyrProGlyGluLeuLeuGln 68
                                                                                                                              3 ValAspHisGluValAsn-----LeuLeuValGluGluIleHisArgLeuGlySer 19
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                                                                                                                                                                                                                                                                                                                                           69 GlyvalHisAspAspValAspIleIleLeuLeuGlnAsp 81
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Matches:
Conservative:
Mismatches:
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ery Match:
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arch completed: March 17, 2004, 16:46:52 b time : 274 secs

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OTHER INFORMATION: in equals a, c, c, correction: (1349473)...(1349473)...(1349473)...(1349473)...(1349473)...(1349473)...(1349473)...(1349473)...(13494710)... equals a, t, c, correction: (1349491)...(1349491)...(1349491)...(1349491)...(1349491)...(1349491)...(1349491)...(147091)...(14

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NAME/KEY: misc\_feature LOCATION: (1310988). OTHER INFORMATION: n equals a, t, NAME/KEY: misc\_feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, t,

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OTHER INFORMATION: n equals a,

c, or g

NANE/KEY: misc\_feature LOCATION: (1664854)..(1664855) CTHER INFORMATION: n equals a, t, 08-916-4218-1

## GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

protein - nucleic search, using frame\_plus\_p2n model

1 on:

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mmand line parameters:

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DEL=frame+ p2n.model - DEV=xlh

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MMAP - LAAGEQUERY - NEG SCORES=0 - WAIT - DSPBICOR=100 - LONGLOG

SV TYREOUT=120 - WARN TIMEOUT=3 0 - THRADS=1 - XGARPOS=10 - LONGLOG

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March 17, 2004, 16:42:09; Search time 2808 Seconds (without alignments) 1250.280 Million cell updates/sec
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410
1 MNVDHEVNLLVEEIHRLGSK.....PGELLLQGVHDDVDIILLQD 81
                                                                                                                                                                                                                                                                                                          3470272 segs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	14953 Homo sa	2992 Seguenc	6995 Sequence	16682 Homo sa	801 Mus mu	8 06	94 Sequ	39 Mus m	670 Mus mus	.991 Mus mu	34 Seguenc	56 Coturi	99 Dani	69 Danio	08 Human	56 Mus mus	36 Mus musc	Rattus	Rattus	Rattus	Sequen	Arabid	AK062756 Oryza sat	Seprai	sequenc	Arabido	ALLEISES ATABLACES	Lotus	Oryza s	m	853 Rattus	181 Rattus n	BUB	9736 Mus mus	4061 Mus mu	24201 Danio re	1763 Danio re	33858 Zebrafis)	03617 Homo sa	17674 Sequence	92694 Homo s	422 Homo sap	32152 Homo sap.	856 Ното вар
	ID	BC014953	AX456992	AX456995	AF116682	BC039801	AX456990	AX456994	AC107839	AC117670	AF065991	AR379534	AY353856	AY398399	BC053269	AL590308	AC102256	AC102536	AC117858	AC137434	AC129055	AX505660	AY087101	AK062756	BX248390	AX396724	ATT16L1	ATCHRIV79	\$5055000 \$5006357	AC097277	AF336113	AC136853	AC114181	AC129212	AC099736	AF504061	BX324201	BX571763	AL953858	AF503617	AX747674	AK092694	747	30345	AP000856
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ALIGNMENTS

RESULT 1

us-09-648-310-4.pzn.rge

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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

It (bases 1 to 74)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F.; Jordan, H., Morce, T., Wang, J., Hsieh, R.,

Hopkins, R.F., Jordan, H., Morce, T., Wang, J., Hsieh, R.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

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Faloy, J., Helton, E., Garcia, A.M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Bouffard, G.G., Blakesley, R.W., Young, A.C., Shevchenko, Y.,

Bouffard, G., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

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CONTACT: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bogos.Do.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisias Prabhu, Parvanch Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Mirandad Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
              Homo sapiens chromosome 6 open reading frame 115, mRNA (cDNA clone open 12978 IMAGE:4849571), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2. (bases 1 to 743)
Strausberg.R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                        BC014953
BC014953.1 GI:15928976
                                                                                                                                                                                                                                                Homo sapiens (human)
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OMMENT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: a Column: 8.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Progression suppressed gene 13 (psgen 13) and uses thereof
Patent: WO 0216419-A 3 28-FEB-2002;
The Trustees of Columbia University in the City of New York (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr
                                                                                                                                                                                                                                                                                                             1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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AX456992.1 GI:21715784
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Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               [1]
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
Liu M., He F.; Furtional prediction of the coding sequences of 121 new genes deduced by
analysis of CDNA clones from human fetal liver";
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted (24-DEC-1998) to the EMBL/GenBank/DDBJ databases.
Department of Experimental Hematology, Institute of Radiation Medicine,
Beijing Taiping Road 27, Beijing 100850, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luo
                                                                                                                                                                                                                                                                                                                                                                                                                                        1-876
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S.,
Liu M., He F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .VGTLKAAKRRKIVTYPGELLLQGVHDDVDIILLQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 G; 245 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                        Last updated, Version 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                             standard; mRNA; HUM; 876 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-648-310-4 (1-81) x AF116682 (1-876)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                            (Rel. 63, Created)
(Rel. 67, Last upd
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Best Local Similarity:
                          437 GAT 439
81
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81 Asp
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09-MAY-2001
                                                                                                                                   AF116682.1
                                                                                                          AF116682;
                                                                               AF116682
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DB:
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                                                                                 256
                                                                                                                                      316
                                                                                                                                                                                         376
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                         21 AsnalaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
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Progression suppressed gene 13 (psgen 13) and uses thereof
Patent: WO 0216419-A 6 29-FEB-2002;
The Trustees of Columbia University in the City of New York (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA
                                                                       257 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGAAATGTGCC
                                                                                                                                                                                  61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln
                                                                                                                                                                 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr
                                                         1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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Conservative:
Mismatches:
Indels:
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Sequence 6 from Patent W00216419.
AX456995
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                             .09-648-310-4 (1-81) x AX456992 (1-835)
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clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 83 Row: h Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="RVQGSDPRSSSSSVKKBAIGESAMNVEHEVNLJVEEIHRLGSKN
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QD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 AATGCTGATGGAAATTAAGTGTGAAGTTTGGGGTCCTCTTCCAGGATGACAGATGTGCC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 ATGAATGTGGAACATGAAGTTAACCTCCTGGTGGAGGAAATTCATCGCCTGGGTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln
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                                                                                                                                              Location/Qualifiers

1. 526

1. 526

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Matches:
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Best Local Similarity:
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Pred. No.:
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

1 (bases 1 to $26)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausnar, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Scheetz, T.E., Borwatseln, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Youchman, J.W., Green, E.D.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Bouterfield, Y.S., Krzywinski, M.I., Skalska, U., Sanilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

NEZ388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC039801 526 bp mRNA linear ROD 16-APR-2003
Mus musculus RIKEN cDNA 3110003A17 gene, mRNA (cDNA clone
IMAGE:1448067), partial cds.
                                                                                                                  255
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Direct Submission
Submitted (12-NOV-2002) National Institutes of Health, Mammalian
Submitted (12-NOV-2002) Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
Tissue Procurement: Marcello Bento Soares, Dh.D.
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Prizayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
http://www.systemsbiology.org
Anup Madan, Jessica Fahay, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                        21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla
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Mus musculus
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AUTHORS
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REMARK

JOURNAL

TITLE

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URCE Rattus sp.  ORGANISM Rattus sp.  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;  Rattus.  FERENCE 1  AUTHORS Fisher, P.B., Kang, D.C. and Su, Z.Z.  TITLE Progression suppressed gene 13 (psgen 13) and uses thereof	O O	ignment Scores: 5.38e-43 Length: 780 ed. No.: 390.00 Matches: 76 rcent Similarity: 98.77% Conservative: 4 r. Local Similarity: 93.83% Manatches: 1 ery Match: 65.12% Indels: 0 : 64.10.4 (1-81) x xx456990 (1-780)		230 AATGCGATGGGAAACTGAAGTTTGGGGTCCTCTTCCAAGACGACAGTGCC 289 41 ASDLeupheGlublaLeuvalGlyThrLeuLysAlablaLysArgArgLysIleValThr 60 41 ASDLeupheGlublaLeuValGlyThrLeuLysAlablaLysArgArgLysIleValThr 60 59 AATCTCTTTGAAGGGTTGGTGGAACTCTGAAAGCGAAAACGAAGGAAG		SULT 7 456994 456994 AX456994 AX456994 FINITION Sequence 5 from Patent W00216419. CESSION AX456994 RESION AX456994.1 GI:21715785 RESION AX456994.1 GI:21715785	<pre>URCE</pre>	AUTHORS FISHER, P.B., Kang, D.C. and Su, Z.Z. AUTHORS FISHER, P.B., Kang, D.C. and Su, Z.Z. TITLE Progression suppressed gene 13 (psgen 13) and uses thereof JOURNAL Patent: WO 0216419-A 5 28-FBB-2002; The Trustees of Columbia University in the City of New York (US) 3ATURES SOURCE 1. 780	/organism="Rattus sp." /mol_type="unassigned DNA" /db_xref="taxon:10118"	lignment Scores: 5.38e-43 Length: 780

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Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galgan, J., Gardyna, S., Gord, S., Carham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liud, G., MacDean, C., Retta, R., Rise, C., Roerson, K., Raymond, C., Spencer, B., Stander, Thoman, N., Stojanovic, N., Talamas, U., Lesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vale, M., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 107626 107725; gap of 100 bp 107726 11441: contig of 107625 bp in length 111542 120063: contig of 8522 bp in length 111542 120063: contig of 8522 bp in length 115064 120163: gap of 100 bp 115064 15088: contig of 9534 bp in length 115074 161248: contig of 9534 bp in length 115074 161248: contig of 9534 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project Indomation
Center project name: 120600
Center project name: 284_Kl
Center project name: 284_Kl
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 169804 bases at least Q20
Consensus quality: 170139 bases at least Q20
Insert size: 170000; agarose-fp
Construct size: 170482; sum-of-contigs
Quality coverage: 13.6 in Q20 bases; sum-of-contigs
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HTG.

Mus musculus (house mouse)

Mus musculus (bouse mouse)

Mus musculus (bouse mouse)

Mus musculus (bouse)

Mus musculus (bosoutia) Sciurognathi, Muridae, Murinae, Mus.

Eukaryota, Metazas, Chordata, Sciurognathi, Muridae, Murinae, Mus.

Elizen, B., Nusbaum, C. and Lander, B.

Mus musculus chromosome 7, clone RP23-383Pll

Lupublished

E (bases 1 to 219661)

Stren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Basten, W., Collins, S., Collymore, A., Chazan, C., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gorde, S., Gorde, M., Callins, E., Grand-Pierre, N., Galdad, J., Machen, E., Landers, T., Lehoczky, J., Levine, I., Johnson, R., Liu, G., Landers, T., Lehoczky, J., Levine, R., Lindblad, Toh, K., Liu, G., Macclean, C., Macchan, P., McErnan, R., Marphy, T., Marquis, N., Mathews, C., Norman, C. H., O'Conner, T., O'Donnell, P., O'Donnell, P., O'Donnell, P., O'Donnell, P., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Ribeback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rise, C., Rogov, P.,
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Remain S. Resertin, M. Roya, M. Schoole, R. Schoole-flowing I. Schoole
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(bases 1 to 786)

Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.

Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 79 19-AUG-2003;
Submitted (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC at Brooklyn, 450 Clarkson Avenue, Brooklyn, NY 11203, USA Location/Qualifiers
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Sequence 79 from patent US 6607879.
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1. 786
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                US-09-648-310-4 (1-81) x AF065991 (1-692)
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AR379534
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Ganguly, K., Yang, L.F. and Reddy, F.K.
A novel CDNA clone from mouse thymus cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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Mismatches:
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                                                                                                                                                                                                      /rpt_family="LiM4"
complement(22572, .23474)
/rpt_family="LiR2_RN"
/rpt_family="LiR2_RN"
/rpt_family="LiR2_RN"
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Matches:
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Ganguly, K., Yang, L.F. and Reddy, P.K.
Direct Submission
                                                                         a./37, .21804
/rpt family="(TCTA)n"
complement(22169, .22245)
/rpt family="LIM4"
22246. .2230
                                                                                                                                                                                                                                                                                              /rpt_family="RMER1B"
2682B. .27000
              /rpt_family="RSINE1"
complement(20062, 20271)
/rpt_family="B3"
21088, 21508
                                                                                                                                                                /rpt_family="(TCTA)n"
complement(22305, .22424)
/rpt_family="Bl_MM"
complement(22425, .22500)
      complement (19343. .19458)
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                                                            rpt family="RLTR10C"
                                                                                                                                                                                                                                                                                                                                                    /rpt_family="(TG)n"
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complement(24373.
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Mus musculus
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AF065991
AF065991.1 GI:16303306
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/tissue type="kidney marrow"
1. .1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
/mol_type="mRNA"
/db xref="taxon:7955"
                             US-09-648-310-4 (1-81) x AY353856 (1-892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200025, P. R. China
Location/Qualifiers
1. .1283
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AY398399.1 GI:37681908
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Mott,I.W. and luvarie,R.D.
CDNA array analysis of lines of Japanese quail divergently selected for four-week body weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/codon_start=1
/product==not experimental
/product="hypothetical protein"
/protein_id="hypothetical protein"
/protein_id="hypothetical"
/prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4Y353856 892 bp mRNA linear VRT 25-AUG-2003 Coturnix coturnix clone QE8f315 hypothetical protein mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                             200 AATGCTGATGGAAAGTTAAGCCGTGAAATTTTGGGGTCCTCTTCCGTGATGATAAATGTG 259
                                                                                                                                                                                                                                                                                                                                                                               260 ccaaccretrigaagcarriggraccaacretraagcrecaaaaccaaaggarrigra 319
                                                                                                                             1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                                                                                                                              40 laAsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAla-LyaArgArgLysIleVal 59
                                                                                                                                                                                                                            21 AsnAlaAspGlyLysLeuSer-ValLys-PheGlyValLeuPheArgAspAspLysCysA 40
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Coturnix.
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Mott.1.W, and Ivarie,R.D.
Direct Submission
Submitted (29-UUL-2003) Genetics, University of Georgia, Green
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/mol_type="mRNA"
/db_xref="taxon:9091"
/clone="QE8f315"
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[85, .51]
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Location/Qualifiers
                                                                            09-648-310-4 (1-81) x AR379534 (1-786)
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AY353856.1 GI:33946397
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psty Match:
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/translation="MNVEHEVSLLIDEIRRIGSKNADGKTSVKFGVLFNDDQCANLFE
ALVGTLKAAKRKVITFDGELLLQGVHDNVDVVLLQD"
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326 AATGCCGATGGACAAGTGAGTGTGAAATTTGGTGTGCTCTTCGCTGATGAAAAGTGTGCC 385
                                                                                                                                                                                                                                                                                                                                                              386 AACCTCTTTGAAGCCCTGGTGGGAACTCTTAAGGCTGCAAAACGACAAAGATTGTCACT 445
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (bases 1 to 1283)
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Deng,M., Zhang,G.W., Sheng,Y., Chen,Y., Ranki,J.P., Look,A.T. and Chen,Z. Gene,Expression Profiling in the Zebrafish Kidney Marrow Tissue
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Direct Submission

Submitted (24-SEP-2003) State Key Lab for Medical Genomics, Shanghai Institute of Hematology, Ruijin Hospital Affiliated to Shanghai Second Medical University, 197 Rui Jin Road II, Shanghai
                                                                                                                                                21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                        41 AsnleuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
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/produce=nhypothetical protein PRO2013"
/protein_id="AAQ97832.1"
/db_xref="GI:37681909"
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us-09-648-310-4.p2n.rge

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Percent Similarity:
Best Local Similarity:
Query Match:
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Gyprinidormes; Cyprinidae; Danio.

Gyprinidormes; Cyprinidae; Danio.

I (bases 1 to 1315)

Strausberg, R. L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Alaschul, S.F., Zeeberg, B., Buetow, K.H., Schemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Abramson, R.D., Mullahy, S.J., Bodask, S.A., McEwan, P.J.,
McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skaleka, U., Smailus, D.E.,
Schent, J.B., Mashey, M., Touchman, J.W., Genen, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and intial analysis of more than 15,000 full-length
human and mouse cDNs Sequences

NED Proc. Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRT 05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                      21 AsnalaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                   41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-UNN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1315 bp mRNA linear Danio rerio cDNA clone IMAGE:6796802, partial cds. BC053269 1 GI:31418949
4 4 0 0
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Conservative:
Mismatches:
Indels:
                                                                                                       3-09-648-310-4 (1-81) x AY398399 (1-1283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Danio rerio (zebrafish)
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85.61%
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ircent Similarity:
ist Local Similarity:
lery Match:
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AUTHORS
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Tissue Procurement: Leonard I. Zon, M.D.

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Sequencing of the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: http://www.shgc.stanford.edu

contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL590308 100296 bp DNA linear PRI 03-JUL-2001
Human DNA sequence from clone RPI1-501K14 on chromosome 6, complete
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
507 TTCGATGGGAGCTGCTACTGCAAGGAGTTCACGACAACGTTGATGTCGTATTACTGCAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AsnalaAspGlyLysLeuSerVallysPheGlyValLeuPheArgAspAspLysCysAla 40
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Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 100296)
Blakey, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                                                                                                      clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 117 Row: m column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 ATGAATGTGGAACATGAAGTCAGTCTGCTCATTGATGAAATCCGCCGACTGGGAGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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/mol type="mgNA"
/db_xref="taxon:7955"
/clone="IMAGE:6796802"
/tissue_type="Kidney, zebrafish"
/clone_Iib="NCI CGAP_ZKid1"
/lab_bost="DHIGE"
/note="Vector: pCMV-SPORT6.1"
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Matches:
Conservative:
Mismatches:
Indels:
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1. .1315
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HTG.
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Direct Submission

AL Chail Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone
requests: clonexequest@sanger.ac.uk
cB10 15A, UK. E-mail enquiries: hunguery@sanger.ac.uk Clone
requests: clonexequest@sanger.ac.uk
requests: clonexequest@sanger.ac.uk
con Jul 4, 2001 this sequence version replaced gi:14252463.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
rogether with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
one plasmid subclone or more than one Mis subclone; and the
assembly was confirmed by reserviction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: SMISSPROT; Tr:, TREMBL; Wp:, WORMEPP: Information on the WORWEPP
Httn://www.sanger.ac.uk/Drone/Alanata/wormen mit or controled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Cettre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/Hgpt/Chr6
RPII-501Ki4 is from the library RPCI-II.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP11-501K14 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-501K14 is at 1 in this sequence. The true left end of clone RP1-225E12 is at 98297 in this sequence. The true right end of clone RP1-94L3 is at 97304 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90. .265
note="MER47 repeat: matches 2242. .2317 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER47 repeat: matches 2242. .2323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ii65. .6268
note="L2 repeat: matches 2607. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 2587. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="MIR repeat: matches 103. .194 of consensus"
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note="Aluðb repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420. .1737
note="AluJb repeat: matches 2. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550. .2961 and the straight of consensus and emblast repeat: matches 3. .306 of consensus."
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note="MER47 repeat: matches 1. ,79 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="MIR repeat: matches 7. .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   010. 2033
note="12 copies 2 mer tt 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="6"
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1503. .9696
Thote="Aludo repeat: matches 90. .281 of consensus"
7703. .10428
Thote="LIMB8 repeat: matches 5126. .5867 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Sequence from overlapping clone RP11-9413 (1619103). Assembly confirmed by restriction digest." 0025. .20120
                                                                             1209. .9497
'note="LIMBB repeat: matches 5863. .6175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10058. .20117
Inote="20 copies 3 mer gcg 73% conserved"
1404. .21522
Inote="MER46C repeat: matches 82. .191 of consensus"
11843. .22026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluJb repeat: matches 129. .279 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thote="AluSg repeat: matches 21. .308 of consensus"
15735
15735
15736
16229. "15532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote="L2 repeat: matches 2351. .2547 of consensus"
2027. .2320
Anote="AluJb repeat: matches 1. .297 of consensus"
2231. .23369
Anote="L2 repeat: matches 2547. .2593 of consensus"
22394. .22607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18247. .18407
/note="MBK58C repeat: matches 40. .88 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="6 copies 8 mer gaaagaaa 79% conserved"
33030. .23106
note="L2 repeat: matches 2667. .2749 of consensus"
3146. .23213
                                                                                                                                                                                                                                                                                                                                                                          1051. .11360

"note="Aluga repeat: matches 1. .310 of consensus"

11361. .12691

//note="L2 repeat: matches 962. .2419 of consensus"

12850. .13009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MER6 repeat: matches 799. .865 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LTR38 repeat: matches 46. .611 of consensus"
'note="MIR repeat: matches 14. .151 of consensus" 8899. .8959 note="MIR repeat: matches 194. .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0429 10759 note="AluJb repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="AluJb repeat: matches 3. .311 of consensus"
2982. .23029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .312 of consensus"
25107. .25470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5295. .15341
note="WIR repeat: matches 97. .142 of consensus"
5342. .15632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8586. .18687

note="MIR repeat: matches 48. .149 of consensus"

9512. .20572
                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 821. .962 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 32. .247 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LTR38 repeat: matches 3. .98 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="4 copies 24 mer 72% conserved" 0058. .20117
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lote="L2 repeat: matches 2616. .2717 of consensus"
1325. .39632
                                                                                                                                                                                                                                                                                                                                                                                                                               .122. .38421
|ote="AluSx repeat: matches 11. .310 of consensus"
                                                                                                                                                                                                                                                                                                           note="1.1uSp repeat: matches 6. .302 of consensus"
3584. 35496
3584. 35496
3588. 36686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Aludo repeat: matches 4. .310 of consensus" 0283. .40636
                                                                                                                                                                                                                                                                                                                                                                                                            ote="MIR repeat: matches 211. .250 of consensus"
3122. .38421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="THE1A repeat: matches 1. .353 of consensus"
note="THEIC repeat: matches 1. .370 of consensus"
5474. .27051
                          5474. .27051
note="THEIC-internal repeat: matches 5. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                       ote="7 copies 8 mer tecttect 75% conserved"
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<sup>21</sup> AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40

<sup>74928</sup> AACCICITIGAAGCAITGGIAGGAACICITAAAGCIGCAAAAGGAAGGAAGAITGIAACA 74987 9 TyrproglyGluLeuLeuLeuGlnGlyValHisAspAspValAsplleileLeuLeuGln 80 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 61

<sup>81</sup> Asp 81

<sup>75048</sup> GAT 75050

earch completed: March 17, 2004, 17:31:12 ob time : 2858 secs

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Sequence 21733, A Sequence 56189, A Sequence 56189, A Sequence 56189, A Sequence 2605, App Sequence 19867, A Sequence 19867, A Sequence 1987, A Sequence 318, App Sequence 1190, App Sequence 1202, A Sequence 1489, A Sequence 2801, App Sequence 281, App Sequence 2830, App Sequence
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US-10-085-783A-21733
; Sequence 21733. Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: Chondarcene Inc.
; APPLICANT: Chondarcene Inc.
; APPLICANT: Chiev. C.C.
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
; FILE REFREENCE: 231/2002
; CURRENT FILING DATE: 2002-02-28
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; RIOR APPLICATION NUMBER: US 60/271,955
; RIOR APPLICATION NUMBER: 3061-03-12
; RIOR APPLICATION NUMBER: 3061-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PATENTIN Version 3.2
; SEQ ID NO 21733
2 US-10-085-783A-21733

2 US-10-242-535A-21733

2 US-10-242-535A-21733

2 US-10-242-535A-5189

0 US-09-245-6189

1 US-09-245-6075

1 US-09-348-842A-355

1 US-09-398-842A-355

1 US-09-398-842A-359

1 US-09-398-842A-359

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1 US-10-282-122A-1488

1 US-10-282-122A-31497

1 US-10-369-493-44316

1 US-10-369-493-44316

1 US-10-369-493-44316

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1 US-09-973-367C-230

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US-10-027-632-267226
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DEL=frame+ pan.model -DEV=xlh

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3=Published Applications NA -OFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1

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| cgn2_6/prodata/1/pubpna/USOE_NEW PUB.seq:*
| cgn2_6/prodata/1/pubpna/USOE_NEW PUB.seq:*
| cgn2_6/prodata/1/pubpna/USOE_DUBCOMB.seq:*
| cgn2_6/prodata/1/pubpna/USOF_PUBCOMB.seq:*
| cgn2_6/prodata/1/pubpna/USOP_NEW PUB.seq:*
| cgn2_6/prodata/1/pubpna/USOP_PUBCOMB.seq:*
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                                                                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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| LOCATION: (48) ...(48)
| OTHER INFORMATION: n is a, c, g,
| FBATURE:
| NAME/KEY: misc_feature
| LOCATION: (328) ...(328)
| OTHER INFORMATION: n is a, c, g,
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; ORGANISM: Human
US-10-085-783A-56189
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Sequence 21731, Application US/10242535A
Sequence 21731, Application US/10242535A
Sequence 21731, Application US/20040013663A1
GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE OF INVENTION: Compositions US/2002-09-12
PRIOR APPLICATION NUMBER: US 60/205, 340
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275, 017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271, 955
PRIOR FILING DATE: 2001-03-12
PRIOR FILING 
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100-085-783A-56189

15 Sequence 56189, Application US/10085783A

15 Sequence 56189, Application US/10085783A

16 Sequence 56189, Application No. US20040037841A1

17 Sequence 56189, Application No. US20040037841A1

18 APPLICANT: ChondroGene Inc.

18 APPLICANT: US 002-02-28

18 PRIOR PELLING DATE: 2001-07-13

19 PRIOR FILING DATE: 2001-07-13

19 PRIOR FILING DATE: 2001-02-28

19 PRIOR FILING DATE: 2001-02-28

19 PRIOR FILING DATE: 2001-02-28

10 WIMBER OF SEQ ID NOS: 56994

10 SOFTWARE: Patentin version 3.2

10 SEQ ID NO 56189

10 LENGTH: 483

10 LENGTH: 483
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MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20	81 AIGAAIGIGGAICACGAGGITAACCICTIAGIGGAGGAAATTCATCGITIGGGILCAAAA 1*0	21 AsnalaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40  141 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTCCGTGATAAATGTGCC 200  41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60  201 AACCTCTTGAAGCATTGGTAGAAACTTTAAAGCTGCAAAAGGAAGG	10-242-535A-56189 10-242-535A-56189 10-quence 56189, Application US/10242535A 10-quence 56189, Application US/10242535A 10-blication No. US20040013663A1 1ENERAL INFORMATION: APPLICANT: Chondrodene Inc. APPLICANT: Liaw, C.C. TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis FILE REFRENCE: 4231/2002 CURRENT APPLICATION NUMBER: US 10/085,783 PRIOR APPLICATION NUMBER: US 60/305,340 PRIOR FILING DATE: 2002-02-28 PRIOR FILING DATE: 2001-03-12 PRIOR FILING DATE: 2001-03-13	ignment Scores: 3.73e-58 Length: 483 ore: 410.00 Matches: 81 rcent Similarity: 100.00% Conservative: 0 st Local Similarity: 100.00% Mismatches: 0 ery Match: 150.00% Gaps: 0	MethanvalAsphisGluvalAsnLeuLeuvalGluGluI

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O9-925-300-545
iequence 545, Application US/09925300
atent No. US20020151681A1
application US/09925300
atent No. US20020151681A1
application Steve Ruben
APPLICANT: Craig Rosen,
APPLICANT: OF INVERT: DO10-09-00
RUGARENT FILING DATE: 2001-08-10
RIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1899
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 545
LENGTH: 778
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (641)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (652)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SULT 6
-09-918-995-26075
-09-918-995-26075, Application US/09918995
spublication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: HYBER INC.
ATTLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   778
81
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-09-938-842A-355
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           Query Match:
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Sequence 19867, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUCLEIC Acid Molecules Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 19867
LENGTH: 533
LENGTH: 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGAAATGTGCC 350
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Conservative:
Mismatches:
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|S-10-425-114-19867
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26075
LENGTH: 458
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OTHER INFORMATION: n = A,T,C or G
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295.00
83.54%
72.15%
                                                                                                                                                                                                                                           NAME/KEY: misc feature
                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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st Local Similarity:
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ORGANISM: Zea mays
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wing
APPLICANT: Wing
APPLICANT: Wing
APPLICANT: Wing
APPLICANT: Wing
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPIJOG-3
CURRENT APPLICATION NUMBER: US 6/9/938,842A
CURRENT FILING DATE: 2000-08-24
PRIOR PILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICANTON NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                       126 cagcccdarddcrcrracaagardadrrrrddcdrcrrcrrcaacaacaacaacaagardda 185
                                                                                                                                                                                                                                                                                                                                                                                     186 AATATCTTTGAAGCACTAGTTGGCACCTTGAGGCCGCCAAGAAGAGGAAGATCTTGACC 245
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Matches:
Conservative:
Mismatches:
                                                                          US-09-648-310-4 (1-81) x US-10-425-114-19867 (1-533)
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; Sequence 355, Application US/09938842A
; Patent no. US20020160378A1
; GENERAL INFORMATION:
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286.00
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Best Local Similarity:
Query Match:
DB:
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Sequence 94878. Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-2163233B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
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                                                         APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2026 (PARA-015PRV)
CURRENT APPLICATION NUMBER: 05/09/770,961
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR APPLICATION NUMBER: 60/178,466
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Mindows Version 4.0
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LOCATION: (1)..(716)

POTHER INFORMATION: unsure at all n locations

PEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_56687C.1

US-10-424-599-94878
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Arabidopsis thaliana
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286.00
80.77%
70.51%
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                  Allen, Keith
Hoffman, Neil
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Best Local Similarity:
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LENGTH: 716
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Pred. No.:
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LENGTH: 492
APPLICANT:
APPLICANT:
APPLICANT:
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                           CHARLA SEA, Application US/09938842A

ublication No. US20040009476A9

ENERAL INFORMATION:

APPLICANT: HALPER, Joef

APPLICANT: HALPER, Joef

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

LENGTH + 486
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Publication No. US20030115639A1
SENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page, Amy
Matthew, Abraham V.
Lefford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
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Rameaka, Joshua G.
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         ULT 9
09-938-842A-355
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APPLICANT:
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100.00%
100.00%
61.46%
Publication No. US20020131971A1 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-099-926-939
                                                                                                                                                                                                                                                       TYPE: DNA
CRGANISM: Homo sapiens
US-10-033-528-939
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Sequence 939, Application US/09920300A
Sequence 939, Application US/09920300A
Sequence 939, Application US/09920300A
GENERAL INFORMATION:
APPLICANT: Magner, Madeleine Joy
APPLICANT: Mu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND SECOLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEC ID NOS: 1789
SOFTWARE: FastSEC for Windows Version 4.0
SEC ID NO 939
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Gaps:
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S-10-033-528-939/c
Sequence 939, Application US/10033528
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ORGANISM: Homo sapiens
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; Sequence 939, Application US/10099926
; Publication No. US20030166064A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Heather
APPLICANT: Meagher, Heather
APPLICANT: Jang, Yudiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE REFERENCE: 210121.547C2
CURRENT APPLICATION NUMBER: US/10/099,926
CURRENT FILING DATE: 2002-03-17
NUMBER OF SEQ ID NOS: 1982
SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 939
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Magher, Madeleine Joy
APPLICANT: Wagher, Madeleine Joy
APPLICANT: Wi, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
TILE REPERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 939
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Sequence 2020, Application US/09294093B
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Sequence 2020, Application US/09294093B
Sequence 2020, Application US/09294093B
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                                                                        552 GICCICITICCGIGALGALGALGAGCAACCTCTTTGAAGCALTGGTAGGAACTCTTAAA 493
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32 ValleuPheArgAspAspLysCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys 51
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ORGNISM: Zea mays
FEATURE:
NAMB/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700345395H1
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Abt10814 H
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Ab176064
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genetic analysis; diagnostic; antisense therapy; gene; ss.
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Thiaglingam A, Lewis ME,
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ABQ56862/c
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DEL=frame+_D2n.model -DEV=xlh

-(cgn2_1/USPTO spool/USO5648310/runat_15032004_101253_16551/app_query.fasta_1.263]

-(cgn2_1/USPTO spool/USO5648310/runat_15032004_101253_16551/app_query.fasta_1.263]

-NGGESEQ_29Jan04 -QFWT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0

DOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi

IST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINO -ALIGN=15

DDE=LOCAL -OUTFWT=pto -NOFM=ext -THR MAX=100 -THR MINEN=0 -MAXLEN=200000000

SER-USO5648310 @CGN 11 1.470 @runat_1803126=50 -NULDN=0 -MAXLEN=2000000000

DMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPELOCK=100 -LONGLG -ICPU=3

O MVAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPELOCK=100 -LONGLG -ICPU=3

TINEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

GAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE_6 -DELEXT=7
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Rat Progr
Human foe
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                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ABQS6106 to ABQ60187 represent isolated nucleic acids (1) differentially expressed in cancer tissues. ABBT8993 to ABBT8004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from the used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of calls in a sample of cells from a patient. (I) is useful for determining the presence of scale other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
tissue type, and in antisense therapy.
                                                                                                      Claim 1; Fig 1; 796pp; English
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Sequence 627 BP; 171 A; 151 C; 153 G; 147 T; 0 U; 5 Other;

Length: 627	Matches: 81	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 0
	410.00 Mat				6 Gap
lignment Scores: red. No.:	core:	ercent Similarity:	est Local Similarity:	sery Match:	3:

3-09-648-310-4 (1-81) x ABQ56862 (1-627)

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271 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 212
                                                                                                          211 AAIGCIGAIGGAAAGIIAAAGCGIGAAAIIIGGGGICCICIICCGIGAIGAIGAAAIGIGC 152
                                                                                                                                                                                                                          TyrFroGlyGluLeuLeuLeuGlnGlyValHisAspAspValAsp1elleuLeuLeuGln 80
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                                                                                                                                                                         21 AsnalaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla
    1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
                                                                                                                                                                                                                                                                       91
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                                                                                                                                                         41
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Query Match:

GAT 29 Asp 81 81

AC66413

AAC66413 standard; DNA; 712

ВР

(first entry) 14-FEB-2001 AAC66413;

Human secreted protein coding sequence SEQ ID NO: 14.

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiolicer; vulnerary; antioorvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiavascular disorder; neurological disease; infection; human; secreted protein; ss.

sapiens Homo WC200058350-A1

RESULT 3

not loale

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The invention relates to the isolation of genes AAC66410-C66458 encoding 49 human secreted proteins AAB32002-B32050. The genes can be used to generate fusion proteins by linking to the gene for the human compared to the human protein as compared to the human protein only. The genes and tission proteins are useful for preventing, ameliorating or treating medical proteins are useful for preventing, ameliorating or treating medical proteins are useful for preventing, ameliorating or treating medical arange of human tissues disclosed in the specification. The nucleic arange of human tissues disclosed in the specification. The nucleic adagnosis, treatment and prevention of: (a) cancer, e.g. breast and cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) anamemia, autoimmune thyroiditis, disbetes mellitus, crohn's disease, anamemia, autoimmune thyroiditis, disbetes mellitus, crohn's disease, multiple sclerosis, theumacoid arthritis and ulcerative collitis, (d) multiple sclerosis, theumacoid arthritis and ulcerative collitis, (d) cardiovascular disorders such as myocardial ischaemias; (d) wound healing (c) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                            Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 241 A; 121 C; 149 G; 201 T; 0 U; 0 Other;
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                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                   22-MAR-2000; 2000WO-US007483
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P-PSDB; AAB32005.
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Best Local Similarity:
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                                                                          26-MAR-1999;
22-DEC-1999;
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Pred. No.:
05-OCT-2000.
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248 308 9 80 40 21 AsnalaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 189 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGCC 41 AsnLeuphedluhlalaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys US-09-648-310-4 (1-81) x AAC66413 (1-712) 369 GAT 371 81 Asp 81 셤 셤 ò В à g à ठ

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BP
'16110
AAF16110 standard; cDNA; 778
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AAF16110;

(first entry) 13-MAR-2001 Human prostate cancer antigen nucleotide sequence SEQ ID NO:545.

neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynacological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss. prostate cancer antigen; detection; diagnosis;

WO200055174-A1. 21-SEP-2000

Homo sapiens.

Not a

08-MAR-2000; 2000WO-US005988

99US-0124270P 12-MAR-1999; (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.

Rosen CA, Ruben SM;

WPI; 2000-587513/55. P-PSDB; AAB56907.

Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer.

Claim 1; Page 1004-1005; 2338pp; English

AAFISSES to AAFISSOS encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AABSG363 to AABS7302. The prostate cancer antigens can have neuroprotective, cyrostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, graaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polymucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAFISSOS to AAFISSOS AABST303 represent sequences used in the exemplification of the present

Sequence 778 BP; 250 A; 151 C; 148 G; 221 T; 0 U; 8 Other;

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-09-648-310-4 (1-81) x AAF16110 (1-778)

Sequence 835 BP; 246 A; 160 C; 176 G; 253 T; 0 U; 0 Other;

Length:

Alignment Scores: Pred. No.:

AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40 21

The invention relates to novel isolated nucleic acids which encode a rat or human Progression Suppressed Gene 13 (PSGen 13) protein. The mucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer. e.g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of the breast, lung, prostate, ovary or colon. PSGen 13 may also be used to suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the coding sequence of human Progression Suppressed Gene 13 (HuPSGen 13) Human, Progression Suppressed Gene 13; rPSGen 13; cytostatic; cancer; blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma; breast; lung; prostate; ovary; colon; gene; ss. 365 246 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGCC 305 09 61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr New rat and human Progression Suppressed Gene 13 for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer. /\*tag= a /product= "Progression suppressed gene 13 protein" Human Progression Suppressed Gene 13 (HuPSGen 13), cDNA. Location/Qualifiers ABK11086 standard; cDNA; 835 BP (UYCO ) UNIV COLUMBIA NEW YORK. Claim 4; Fig 2; 53pp; English. 25-AUG-2000; 2000US-00648310. 27-AUG-2001; 2001WO-US026795. Su Z; (first entry) Kang D, 2002-280914/32. P-PSDB; AAU76533. GAT 428 87 WO200216419-A2 81 Asp Homo sapiens 05-JUN-2002 28-FEB-2002 Fisher PB, ABK11086; 41 908 426 ABK11086 RESULT ò 엄 ò 임 ò 입

us-09-648-310-4.p2n.rng

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Homo sapiens.
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                                                                                                                                        197 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA
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tissues useful for determining the presence of colon cancer in a
tissue type, and in antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, colon cancer, cancer, tissue profiling, forensic, mapping, genetic analysis, diagnostic, antisense therapy, gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer related nucleotide sequence SEQ ID NO:750
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ57055 standard; cDNA; 594 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 796pp; English
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                                                                                      3-09-648-310-4 (1-81) x ABK11086
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Thiaglingam A, Lewis
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                  Similarity:
al Similarity:
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259 AAIGCIGAIGGAAAGITAAGGGGGAAAATTIGGGGICCICTICCGIGAIGAIAAAIGIGC 318
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of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the arresponding gene resides, and in tissue profilling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrProglyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer related nucleotide sequence SEQ ID NO:748
                                                                                                                                                                                                            Sequence 594 BP; 157 A; 142 C; 134 G; 149 T; 0 U; 12 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, colon cancer, cancer, tissue profiling, forensic, m
genetic analysis, diagnostic, antisense therapy, gene, ss
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Matches:
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Thiaglingam A, Lewis ME;
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Best Local Similarity:
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GAA 441
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27-AUG-2001; 2001WO-US026795.

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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78931 to ABB7804 represent proteins encoded by the ABG60776 to ABG60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting and statent sample, and for detecting the presence or absence of a polymucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and antagonists
Claim 1; Fig 1; 796pp; English
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Sequence 717 BP; 192 A; 171 C; 155 G; 180 T; 0 U; 19 Other;

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AACCICITIGAAGCATIGGIAGGAACICTITAAAGCIGCAAAAGGAAGGAAGAIIGIAACA 381
                                                                                                                                                                                                                                                                                                                                                                            382 TATCCAGGAGAGCTGCTTCTACAAGGTGTTCATGATGATGTTGACATTATATTACTGCAA 441
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                                                                                                                                                              1 MetAsnValAspHisGluValAsnLeuValGluGluGluIleHisArgLeuGlySerLys
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            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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st Local Similarity:
ery Match:
ignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "Progression suppressed gene 13 protein"
                                                                                                                                                                                                                                                                                                                  Rat Progression Suppressed Gene 13 (rPSGen 13), cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                      ABK11085 standard; cDNA; 780
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                              blood vessel;
breast; lung;
                                                                                                                                                                                                                                                                                           05-JUN-2002
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SULT 7 K11085

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The invention relates to novel isolated nucleic acids which encode a rat or human progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer. e.g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour mersher, tumour mersateasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the coding sequence of rat Progression Suppressed Gene 13 (rPSGen 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleIleLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 ATGAACGTGGAGCATGAGGTTAACCTCCTGGTGGAGGAAATTCATCGTCTGGGTTCCAAA
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                                                                                                                                                                                      and human Progression Suppressed Gene 13 for preventing the of cancer cells and/or new blood vessels, and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 780 BP; 223 A; 151 C; 187 G; 219 T; 0 U; 0 Other;
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76
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                         growth of cancer cells and/or new
patients suffering from a cancer.
                                                                 (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                           Claim 2; Fig 1; 53pp; English.
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                              25-AUG-2000; 2000US-00648310.
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390.00
98.77%
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                                                                                                                                       WPI; 2002-280914/32.
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Best Local Similarity:
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ID ACH:
XX
AC ACH:
XX
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DT 13-0
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DE Hum:
XX
XW Hum:
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411 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGATGATT 458
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                                                                                                                  ABT10814;
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynuclectide comprising any one of 38043 cDNA sequences, appearing as Aril2789-ARH5081. whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynuclectide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for infernsics, in assessing bloidiversities, or in identifying mutations, responsible for generic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for Chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense by sequences. Note: The greence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
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                                                                                                                                                                                                                                                                                                                                                  Stache-Crain B, Dickson MC, Jones LW;
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Matches:
Conservative:
Mismatches:
Indels:
genome mapping, biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 26075; 44pp; English.
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                                                                                                                                                    30-JUL-2001; 2001US-00918995.
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(STAC/) STACHE-CRAIN B.
(DICK/) DICKSON M C.
(JONE/) JONES L W.
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                                       Homo sapiens.
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The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867.

STILLI2, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients.

The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be the onset or progression of breast cancer. The breast cancer genes may be useful or progression of breast for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the printed specification, but was obtained in electronic format directly from WHOO at the printed pot from the printed pot from the printed profrage sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing breast cancer in a patient comprises detecting the level c
gene expression in cell or tissue samples, where a differential gene
expression is indicative of breast cancer.
                                                                                                                                                                                                                                                                                                                                 Human; breast specific gene; breast cancer; differential expression;
                                                                                                                                                                                                                                                             Human breast cancer associated coding sequence SEQ ID NO: 948.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 948; 260pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 653 BP; 213 A; 135 C; 88 G; 217 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Orr MS, Nation M, Diggans JC, Zeng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-648-310-4 (1-81) x ABT10814 (1-653)
                                                                                                                                                                                                                                                                                                                                                                         cytostatic; gene therapy; gene; ss.
ABŢ10814/c
ID ABT10814 standard; cDNA; 653 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2001; 2001US-0263757P.
25-APR-2001; 2001US-0286090P.
23-MAY-2001; 2001US-0292517P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2002; 2002WO-US002176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.04e-48
380.00
95.06%
93.83%
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-674803/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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AAZ21517 standard; cDNA; 800 BP.

3ULT 10 321517

404 GAT 402

81 Asp 81

61

41

(first entry)

01-DEC-1999

AAZ21517;

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290 AATCTCTTTGAAACCGTTGGTGGGAACTCTGAAAGCCCGCAAAAAGGAAAGAAGATTGTTA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 CGTACGCAGAAGAGCTGCTTTTGCAAGGTGTTCATGATGATGATGTTGATGATGTTGTATTGCTGC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 AATGCCGATGGGAAACTGAGTGTGAAGTTTGGGGTCCTCTTCCAAGACGACAAGATGTGCC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
       requires only a single anchored primer for amplification and reamplified cDNA can be analysed by reverse Northern blotting
                                                                                                                                                                                                                                                                                                                                           1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 AsnLeuPheGluAla-LeuValGlyThrLeuLysAla-AlaLysArgArgLysIleValT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 hrTyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; pathway; promoter; termination sequence; corn; ss.
                                                                    Sequence 800 BP; 243 A; 153 C; 185 G; 219 T; 0 U; 0 Other;
                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays DNA fragment SEQ ID NO: 76053.
                                                                                                                                                                                                                                                                                               US-09-648-310-4 (1-81) x AAZ21517 (1-800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC53910 standard; DNA; 551 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0123180P.
99US-0123548P.
99US-0125788P.
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99US-0131449P.
99US-0132449P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0126264P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127462P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0128234P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0128714P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130449P
                                                                                                                                        2.94e-44
                                                                                                                                                            352.00
93.98%
89.16%
85.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays subsp. mays.
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 lnAsp 81
                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC53910;
                                                                                                                                                                                                                         Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the progression suppressed gene 13 (PSGen13). This gene has suppressed expression in progressed tumour cells. PSGen13 was identified using new methods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction differential RNA display (RSDD) between the two samples to generate two subtraction samples. The subtraction samples to and compared to identify those nucleic acids that are differentially expressed. The method is used to identify and clone differentially expressed genes, particularly those with increased or reduced expression and progressed genes (PSGen) and progressed genes (PSGen). The method reduces the complexity of the band pattern produced in conventional differential RNA display (where bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated, allowing identification and cloning of genes displaying anticipated differential expression. RSDD
                                                                                     524 AACCICITIGAAGCATIGGIAGGAACICITAAAGCIGCAAAACGAAGGAAGATIGIAACA 465
                                                                                                                                                            584 AATGCTGATGGAAAGTTAAGCGTGAAATTGGGGGTCCTCTCCCGTGATGATAAATGTGCC 525
                                         AsnieuPheGluAlaieuValGlyThrLeuLysAlaAlaiysArgArgiysIleValThr 60
                                                                                                                                   TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumor progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Progression suppressed gene, PSGen; progression elevated gene, PEGen, tumour; reciprocal subtraction differential RNA display; RSDD, differential expression; gene cloning; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "PSGen13"
/note= "Progression suppressed gene 13 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Progression suppressed gene 13 (PSGen13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Claim 21; Fig 35B; 110pp; English.

(UYCO ) UNIV COLUMBIA NEW YORK.

WPI; 1999-550872/46.

Fisher PB;

P-PSDB; AAY39325

98US-00032684. 98US-00185115. 98US-00197889. 99WO-US004323.

> 03-NOV-1998; 23-NOV-1998; 27-FEB-1998;

170. .448 /\*tag= a

Rattus sp.

WO9943844-A1

26-FEB-1999;

02-SEP-1999

9US-0132407P 9US-0132484P 9US-0132485P 9US-0132486P 9US-0132487P	900S-01342189 P90S-01342189 P90S-01342189 P90S-0134219 P90S-0134941P90S-0135353 P90S-0135353 P90S-013535 P90S-01355 P90S-013535 P90S-01355 P90S-0135	9US-0136021P 9US-0136392P 9US-0137828P 9US-013722P 9US-0137724P 9US-0137724P 9US-0138640P 9US-0138840P 9US-0138840P 9US-0139113P 9US-0139113P	9UG-0134452P 9UG-01345454P 9UG-01345454P 9UG-0134554P 9UG-0134554P 9UG-0134564P 9UG-013462P 9UG-013462P 9UG-013464P 9UG-013750P 9UG-0139761P 9UG-0139761P 9UG-0139761P	990% 01403539. 990% 01403539. 990% 01403545. 990% 01409239. 990% 01412879. 990% 014218429. 990% 014218429. 990% 01423909. 990% 01423909. 990% 01423909. 990% 01423909.	905-014408659 905-01441259 905-01441319 905-01441319 905-01441319 905-01441359 905-014461529 905-01446149 905-01446149
0-APR-199 4-MAY-199 5-MAY-199 6-MAY-199 6-MAY-199 7-MAY-199	14 MAY - 1999 14 MAY - 1999 14 MAY - 1999 16 MAY - 1999 19 MAY - 1999 21 MAY - 1999 21 MAY - 1999	25-MAY-1999 28-MAY-1999 01-JUN-1999 04-JUN-1999 07-JUN-1999 10-JUN-1999 10-JUN-1999 14-JUN-1999 14-JUN-1999 16-JUN-1999	17 - CUN - 1999 18 - CUN - 1999 21 - CUN - 1999 22 - CUN - 1999	22222220000011111 884890111110089284487	16-001-1999 19-001-1999 19-001-1999 19-001-1999 19-001-1999 20-001-1999 21-001-1999 21-001-1999
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9US-0145088P 9US-0145089P 9US-0145080P 9US-0145080P 9US-0145145P 9US-0145145P 9US-0145128P 9US-0145128P 9US-0145128P 9US-014513P 9US-0145913P	9US-0146981P 9US-0146388P 9US-0146388P 9US-0147038P 9US-0147102P 9US-0147102P 9US-0147303P 9US-0147418P 9US-0147418P 9US-0147418P 9US-01447418P 9US-01447418P 9US-0144741P	905-0146894P 905-01493689 905-01493689 905-0149426P 905-0149723P 905-0149929P 905-0149929P 905-015066P 905-015066P 905-0151066P 905-0151066P 905-0151066P	990%-0152430P-9990%-0152430P-990%-0152430P-990%-0154018P-990%-0154139P-990%-0155486P-990%-0155486P-990%-015568P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-015923P-990%-01592
1-001-199 2-001-199 2-001-199 2-001-199 3-001-199 3-001-199 3-001-199 7-001-199	2. AUG. 1999 2. AUG. 1999 3. AUG. 1999 3. AUG. 1999 4. AUG. 1999 6. AUG. 1999 9. AUG. 1999 9. AUG. 1999 9. AUG. 1999 9. AUG. 1999 9. AUG. 1999 9. AUG. 1999		10.5EP-12999 11.5EP-12999 12.5EP-12999 15.5EP-12999 16.5EP-12999 16.5EP-12999 22.5EP-12999 23.5EP-12999 24.5EP-12999 24.5EP-12999 24.5EP-12999 25.5EP-12999 26.0CT-12999 26.0CT-12999 27.0CT-12999 28.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 29.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20.0CT-12999 20
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BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JAN-2000; 2000US-0178466P
                                                                                                                                                                                                                                         2.26e-34
286.00
80.77%
70.51%
69.76%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
        WPI; 2002-304127/34.
                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE81847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; ss.
                                                                                                                                                                                                                                                                                 Ouery Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE81847/
ID ADE8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                           328
                                                                                                                                                                                                                                                                                                                                     40
                                                                                                                                                                                                                                                                                             1 MetAsnValAspHisGluValAsnLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                                                                                                                                                                            AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                269 AATATCTTTGAAGCACTAGTTGGCACCTTGAGGGCCGCCAAGAAGAGAAGAAGATCTTGACC
                                                                                                                                                                                                                                                                                                                                     21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla
                                                                                                                                                                                                                                                                                                                                                                                                                    TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeu 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana; plant; gene; stress; transgenic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana stress regulated gene SEQ ID NO 355.
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABZ12550 standard; DNA; 486 BP
99US-0160768P.
99US-0160768P.
99US-01607814P.
99US-0160814P.
99US-0160814P.
99US-016088P.
99US-016098P.
99US-016196P.
99US-0161404P.
99US-0161404P.
99US-0161406P.
99US-0161406P.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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71.95%
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                            21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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                                                                                                                                 26-OCT-1999
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29-OCT-1999
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                                                                                                                       26-OCT-1999
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or profile of expressed polynucleotides in the plant cell with an detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ1219-6-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258
Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40
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inhibitor testing; activator testing; modifier testing; fungicide;
insecticide; genetic function; genetic regulation; cellular metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeu 78
                                                                                                      Claim 144; SEQ ID NO 355; 577pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 486 BP; 142 A; 103 C; 116 G; 125 T; 0 U; 0 Other;
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78

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41 AsnieuPheGlualaieuValGlyThrieuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                        61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeu
                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 75315.
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9905-0134370P

9905-0134941P

9905-013523P

9905-0135629P

9905-0135629P

9905-0136232P

9905-0136782P

9905-0136782P

9905-0137528P

9905-0137528P

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9905-0137528P

9905-0137528P
                                                                                                                                             AAC53673 standard; DNA; 657 BP
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99US-0123180P.
99US-0125788P.
99US-0126784P.
99US-0126784P.
99US-0126744P.
99US-0128744P.
99US-0130479P.
99US-0130479P.
99US-0131449P.
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990%-0132485P.
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990%-0132867P.
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25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
21-APR-1999;
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23-APR-1999;
28-APR-1999;
30-APR-1999;
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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19-MAY-1999;
20-MAY-1999;
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10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
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14-MAY-1999;
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24-MAY-1999;
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01-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                          AAC53673;
                                                                                                                    RESULT 14
                                                                                                                                  AAC53673
                                                                                                                                              The invention describes a nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to any one of 999 fully defined Arabidopsis thaliana sequences (I) as given in specification e.g., 360, 1137, 455, 2199, 472 nucleotides, etc., or tis fragment. (I) is useful as a hybridisation probe to complementary molecules in a cDNA library. (I) is also useful for generating genetically modified and transgenic organisms, usually plant cells and plants. A proten encoded by (I) is useful in screening assays to determine the effect of candidate inhibitors, activators or modifiers of the gene product. The protein is also useful for screening biologically active agents e.g., fungicides and insecticides. A genetically modified cell, comprising an exogenous insecticides. A genetically modified cell, comprising an exogenous sequences operably linked to a sequence capable of hybridising under stringent conditions to (I) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene product. This sequence represents an Arabidopsis thaliana polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetasnValaspHisGluValasnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                                                                                                 Yu Y;
TD, Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                          Novel Arabidopsis thaliana nucleic acids useful for generating genetically modified transgenic organisms, for screening biologically active agents such as fungicides, insecticides.
                                                                                                                                                                                                                                                                                                oorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
Rameaka JG, Page A, Mathew AV, Ledford BL, Woesner JP, Haas I
Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
Hurban P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 492 BP; 137 A; 103 C; 101 G; 151 T; 0 U; 0 Other;
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PAGE A.
MATHEW A V.
LEDPORD B L.
WOESSNER J P.
HADAS W D.
CARCIA C A.
KRICKER M.
KRICKER M.
SIATER T.
DAVIS K R.
ALLEN K.
HOFFWAN N.
                                               HAMILTON C M.
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RAINES T M.
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PR 12-AUG-1999; PR 13-AUG-1999; PR 13-AUG-1999; PR 23-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 21-AUG-1999; PR 22-AUG-1999; PR 21-AUG-1999; PR 22-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999	lignment Scores: red. No.: core: ercent Similarity est Local Similar uery Match:
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                                                                             199 ATGAACGTAGACGAAGAGTTCAGAAACTGGAAGAAGAGATCCATCGTCTTGGTTCTCGT 258
                                                                                                                                                                318
                                                                                                                                                                                                                                    20
                                                                                                                      21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                           41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
                                      1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
                                                                                                                                                                  259 cagaccdarddcrcrracaaddrgacgrrriddadrgrrigrricaardacdardriddec
                                                                                                                                                                                                                                                                                                                             TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleLeu 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding colon tumour protein, SEQ ID No 939,
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3-09-648-310-4 (1-81) x AAC53673 (1-657)
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28-MAR-2001; 2001US-0279763P.
29-JUN-2001; 2001US-0302051P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-241739/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200212328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-2002
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                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK45388
                                                                                                                                                                                                                                                                                                                                                                                                         3X45388
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The invention relates to polynucleotides encoding colon tumour proteins. The polynucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polynucleotide sequences may be used as hybridisation probes or primers, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. The compositions are useful for stimulating an immune response against cancer, particularly for the immunotherapy of colon cancer, and as markers for the progression of cancer. ABK4450-610n and an accent coding sequences of human colon tumour proteins of the invention. Note: With the exception of SEQ ID No 1 and 2, the sequence data for this parent did not form part of the printed specification but was supplied by the Buropean Patent Office

Claim 1; SEQ ID NO 939; 147pp; English.

Sequence 552 BP; 190 A; 104 C; 75 G; 183 T; 0 U; 0 Other;

552

Length:

4.84e-29

lignment Scores: red. No.:

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192 GCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCAT 433
                                                                                                                              493
                                                                                                       21
                                                                                                                                                        71
                                                                                                                    52 AlaAlaLysArgArgLysIleValThrTyrProGlyGluLeuLeuLeuGlnGlyValHis
                                                                                                      ValleuPheArgAspLysCysAlaAsnLeuPheGluAlaLeuValGlyThrLeuLys
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           Conservative:
Mismatches:
Indels:
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Matches:
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                                                  Gaps:
                                                                             US-09-648-310-4 (1-81) x ABK45388 (1-552)
252.00
100.00%
100.00%
                                     61.46%
       Percent Similarity:
Best Local Similarity:
Query Match:
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GenCore version 5.1.6  pyright (c) 1993 - 2004 Compugen Ltd.  search, using sw model  th 17, 2004, 11:45:37; Search time 3704 Secon     (without alignments)  9770.905 Million cell  99-648-310-3  goacgaggcttgagcgcagtaaagacatgtaactgt  WITY_NUC  2010.0, Gapext 1.0  20272 segs, 21671516995 residues  s satisfying chosen parameters: 6940544  th: 200000000  th: 2000000000  th: 2000000000  th: 2000000000  th: 20000000000  th: 200000000000  th: 2000000000000000000000000000000000000	GenCore version 5.1.6 (c) 1993 - 2004 Compugen	- nucleic search, using sw model	March 17, 2004, 11:45:37; Search time 3704 (Without alignmer 9770:905 Million	US-09-648-310-3 score: 835 l ggcacgaggcttgagcgcagtaaagacatg	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.	d: 3470272 segs, 21671516995 residue	number of hits satisfying chosen parameters: 694054	DB seq length: DB seq length:	-processing: Minimum Match 0% Maximum Match 100 Listing first 45	GenEmbl:*  1: 9D ba:*  2: 9D_ha:*  4: 9D_ou:*  6: 9D_ou:*  6: 9D_ph:*  9: 9D_ph:*  11: 9D_ph:*  11: 9D_ph:*  11: 9D_ph:*  11: 9D_ph:*  11: 9D_ph:*  12: 9D_ph:*  13: 9D_un:*  14: 9D_ph:*  15: 9D_ph:*  16: 9D_ph:*  17: 9D_ph:*  18: 9D_ph:*  19: 9D_ph:*  10: 9D_ph:*  10: 9D_ph:*  11: 9D_ph:*  12: 9D_ph:*  13: 9D_un:*  14: 9D_ph:*  15: 9D_ph:*  16: 9D_ph:*  17: 9D_ph:*  18: 9D_ph:*  19: 9D_ph:*  10: 9D_ph:*  10: 9D_ph:*  10: 9D_ph:*  11: 9D_ph:*  12: 9D_ph:*  13: 9D_ph:*  14: 9D_ph:*  15: 9D_ph:*  16: 9D_ph:*  17: 9D_ph:*  18: 9D_ph:*  18: 9D_ph:*  19: 9D_ph:*  10: 9D_ph:*  10: 9D_ph:*  10: 9D_ph:*  11: 9D_ph:*  12: 9D_ph:*  13: 9D_ph:*  14: 9D_ph:*  15: 9D_ph:*  16: 9D_ph:*  17: 9D_ph:*  18: 9D_ph:*  18: 9D_ph:*  18: 9D_ph:*  18: 9D_ph:*  19: 9D_ph:*  10: 9D_ph:*	() () () ()
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	DB ID									_				2 AC102536 2 AC107839	$\sim$														_	4				ALIGNMENTS		835 bp DNA from Patent WO0216419.	.715784	lan)	Chordata; Craniata Primates; Catarrhi	.C. and Su.Z.Z.	sed gene 13 A 3 28-FEB-	
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CAGCCGTCTTTCTCTTTGCCTCAGCCACTTCCTTCCTTCGCCTCACCCTCCCCAGTGCAC
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Location/Qualifiers
1. 835
//organism="Homo sapiens"
//mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                    Length 835;
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Larity 100.0%; Pred. No. 1.5e-179;
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Catarrhini, Hominidae, Homo.
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Fisher,P.B., Kang,D.C. and Su,Z,Z.
Progression suppressed gene 13 (psgen 13) and uses
Patent: WO 0216419-A 6 28-FEB-2002;
The Trustees of Columbia University in the City of
Location/Qualifiers
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al Similarity 100.0%; Pred. No. 1.5e-179;
835; Conservative 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
             GI:21715786
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ACCESSION
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Unclassified.
1 (bases 1 to 786)
1 (bases 1 to 786)
Cocks,B.G., Stuart,G.G. and Seilhamer,J.J.
Cockspilions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 79 19-AUG-2003;
Location/Qualifiers
                 66 AGGTAACCGGGTCCAGACCCACGCGCGCGCAGTTCTCCGGCGGGAAAGGAAAACCGGCGCAG
                                                                                                                                                         186 GGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGA
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Pred. No. 1.6e-159;
0; Mismatches 5; Indels
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AR379534
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/organism="unknown"
/mol_type="genomic DNA"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Ouyang S., Luo L., Bi J.,
Liu M., He F., Though Sequences of 121 new genes deduced by
analysis of CDNA clones from human fetal liver";
Unpublished.
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   721 TAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAGCAAACTGAAGAC 780
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Department of Experimental Hematology, Institute of Radiation Medicine,
Beijing Taiping Road 27, Beijing 100850, P. R. China
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                                  781 CAACTCCTATGAGAAATATTATGATGTTTATGTAATAAAGACATGTAACTGTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.3%; Score 762.6; DB 17; Length 876; 99.5%; Pred. No. 4.5e-163; ive 0; Mismatches 4; Indels 0;
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09-MAY-2001 (Rel. 67, Last updated, Version
                                                                                                                                                                                                                                                                                              Homo sapiens PRO2013 mRNA, complete cds
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                                                                                                                                                 AF116682 standard; mRNA; HUM; 876
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Best Local Similarity 99.5
Matches 765; Conservative
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'gene="C6orf115"
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Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 743)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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EFERENCE AUTHORS

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Concact: MGC help desk
Email: Gapbs romail nih gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
Consat: MGC help desk
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
infe@begsc.bc. ca
infe@begsc.bc. ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
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Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M. Soares,M.B. Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninot,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bonaratne,P.H., Richards,S., Worley, K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Wolley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.N., Villalon,D.K., Muzmy,D.M., Sodergren,B.J., Lu,K., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Wilting,M., Madan,A., Young,A.C., Shevcherko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences
12 22388277
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/db_xref="LocusID:58527"
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ALVGTLKAAKRRKIVTYPGELLLQGVHDDVDIILLQD"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
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db_xref="LocusID:58527"
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ALS90308 100296 bp DNA linear PRI 03-JUL-2001
Human DNA sequence from clone RP11-501K14 on chromosome 6, complete
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                                              Gaps
                                                4
        Length 743;
                                            Indels
      Score 698; DB 9; L
Pred. No. 2.3e-148;
0; Mismatches 0;
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          83.6%;
99.4%;
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Query Match
Best Local Similarity 99.4
Watches 712; Conservative
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ORGANISM
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Submitted (03-JTM-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk cn Jul 4, 2001 this sequence version replaced gi:14252463.
During sequence assembly data is compared from overlapping clones.

Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 100296)

Blakey, S. Direct Submission

FERENCE AUTHORS TITLE JOURNAL

MMENT

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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RPII-501K14 is from the library RPCI-II.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBACc3.6
IMPORTANT: This sequence is not the entire insert of clone RPII-501K14 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RPII-505K14 is at 1 in this sequence. The true left end of clone RPII-525E12 is at 98297 in this sequence.

The true left end of clone RPII-94L3 is at 97304 in this sequence.
where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORWHEP; Information on the WORWHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MER47 repeat: matches 2242. .2323 of consensus"
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/note="MER47 repeat: matches 2242. .2317 of consensus"
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92.09. .9497
/note="L1MB8 repeat: matches 5863. .6175 of consensus"
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/note="AluSx repeat: matches 3. .306 of consensus"
577. .895
/note="WIX repeat: matches 21. .166 of consensus"
6062. .6159
/note="LZ repeat: matches 2587. .2709 of consensus"
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/note="12_repeat: matches 2607. .2709 of consensus"
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/note="AluJb repeat: matches 1. .295 of consensus"
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2010. .2033
'note="12 copies 2 mer tt 100% conserved"
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note="MIR repeat: matches 103. .194 of consensus"
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note="MER47 repeat: matches 1. .79 of consensus"
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note="MIR repeat: matches 7. .185 of consensus"
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/note="L2_repeat: matches 1768.
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/clone="RP11-501K14"
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is 90281 of consensus" is 51265867 of consensus" is 1310 of consensus" is 51145126 of consensus"	21962 of consensus 11310 of consens 522419 of consens 129279 of consens 97142 of consens 142250 of consens 143250	s 13 s 12 es 40. 4814 pping c conserv	ches 82191 of consensus"  23512547 of consensus" hes 1297 of consensus" :25472593 of consensus" hes 3247 of consensus" hes 3311 of consensus" 126672749 of consensus" hes 799865 of consensus" hes 398 of consensus" hes 46611 of consensus" hes 2802 of consensus" hes 1312 of consensus" hes 1370 of consensus" hes 1370 of consensus" hes 1369 of consensus"
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75166 74986 75227 TATGATGCTATAAATAATACCTATTATTTTTCTCAGGAATCTGGTTAGGAATTGCAGGC 75286 74867 AGATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGC 74926 75047 AGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTGTTTTCTGGTAAACTGGAA 75106 ò 375 435 TATAAAGTGAAAGAACATTTGAACATACTTAATGTATTTTATAGAACTTTGTAAA 555 615 315 495 675 28722. .29939
/note="Linual repeat: matches 5302. .6111 of consensus"
29400. .29708
/note="Linual repeat: matches 1. .310 of consensus"
29709. .29861
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30862. .31350
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31360. .31887
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32357. .32689
/note="Linual repeat: matches 31. .444 of consensus"
32948. .33222
/note="Linual repeat: matches 31. .286 of consensus"
/note="Linual repeat: matches 31. .286 of consensus"
/note="Linual repeat: matches 31. .286 of consensus" 256 AAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGC ATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGACATTATATTACTGCA 436 AGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTGTTTCTGGTAAACTGGAA CTCAGGAATCTGGTTAGGAATTGCAGGC 0; Gaps 78122. .38421 /note="Alusx repeat: matches 11. .310 of consensus" /note="L2 repeat: matches 2616. .2717 of consensus" 39325. .39632 /note="Alus repeat: matches 4. .310 of consensus" /note="Alus repeat: matches 1. .353 of consensus" /note="THELA repeat: matches 1. .353 of consensus" //note="MiuSp repeat: matches 6. .302 of consensus"
35384. .35496
//note="MIR repeat: matches 32. .147 of consensus"
35388. .3686
//note="Mlusx repeat: matches 1. .302 of consensus"
37165. .37220 7227 .37266 note="MIR repeat: matches 211. .250 of consensus" 3717. .34028 note="AluY repeat: matches 1. .310 of consensus" 4911. .35200 repeat: matches 1. .309 of consensus" Query Match 69.3%; Score 578.4; DB 9; Length 100296; Best Local Similarity 99.8%; Pred. No. 5.2e-121; Matches 579; Conservative 0; Mismatches 1; Indels 0; C TATGATGCTATAAAATAAATCCTATTATTT repeat\_region 376 496 556 616 919 à g g 8 8 8 음 상 음 ò a  $\delta$ 유  $\delta$ 

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PAT 10-JAN-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Memo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="tunassigned DNA"
/db xref="tuxon:9606"
/noTe="EMBL/GenBank Accession No. AA287347"
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45.8%; Score 382.4; DB 6;
Best Local Similarity 99.7%; Pred. No. 1.6e-76;
Matches 383; Conservative 0; Mismatches 1;
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AX341854.1 GI:18137836
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WO0229103.
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     TATAGATATTTGACATTCTGCGAAAGCAACAAGCAAACTGAAGACCAACTCCTATGAGAA 795
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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King, G.E., Meagher, M.J., Xu, J. and Secrist, H.
Compositions and methods for the therapy and diagnosis of
cancer
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CORIXA CORPORATION (US)
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Progression suppressed gene 13 (psgen 13) and uses thereof Patent: WO 0216419-A 1 Z8-FBR-2002;
The Trustees of Columbia University in the City of New York Location/Qualifiers
1. 780
| ... 780
| /organism="Rattus sp."
| /mol_type="unassigned DNA"
| /db_xref="taxon:10118"
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69.1%; Pred. No. 9.4e-66;
iive 0; Mismatches 218;
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Jiang,Y., Harlocker,S.L. and Secrist,H. Compositions and methods for the therapy cancer Patent: WO 0196388-A 2101 20-DEC-2001; CORIXA CORPORATION (US) Location/Qualifiers
                                                                                                                                       Query Match 43.7%; Score 365.2; DB 6; Best Local Similarity 99.2%; Pred. No. 1.3e-72; Matches 365; Conservative 1; Mismatches 2;
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sciurognathi, Muridae, Murinae,
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Progression suppressed gene 13 (psgen 13) and uses 1
Patent: WO 0216419-A 5 28-FEB-2002;
The Trustees of Columbia University in the City of 1
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                                                                      A nover Unpublished A nover Unpublished Compublished to 692)
2 (Dases I to 692)
Ganguly,K., Yang,L.F. and Reddy,P.K.
Direct Submission Submitted (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Submitted (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Submitted (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY HSC Direct Computer (15-MAY-1998) Anatomy & Cell Biology, SUNY Biology, SUNY Biology, SUNY Biology,
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1 (bases 1 to 692)
Ganguly,K., Yang,L.F. and Reddy,P.K.
A novel cDNA clone from mouse thymus cDNA library
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/tissue_type="thymus"
<1. 240
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Best Local Simil
Matches 494; (
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1. .296
/organism="Homo sapiens"
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99.3%;
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Best Local Similarity 99.3
Matches 290; Conservative
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                                           C12N5/10,
PC C12P21
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Expressed sequence tags and encoded human proteins
Patent: EP 1033401-A 34272 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 296;
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Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 30188 02-OCT-2001;
GENSET
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                                                                                             296 bp DN Sequence 34272 from Patent EP1033401. AX918409
CATGAAAATGTTGTTGTTATGGAATAAAAA
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/db_xref="taxon:9606"
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26-FEB-1999 US 60/122487
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JP 2001269182-A/30188
02-OCT-2001
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                                                                                                                                              AX918409.1 GI:40212198
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Eukarotain Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Bukarota; Metazoa: Rodentia; Sciurognathi; Muridae; Murinae; Mus. Bukarota; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 526)

1 (bases 1 to 526)

2 Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore-T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheerz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.C., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKerran, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Murny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hallon, D.K., Murny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiling, M., Madan, A., Coung, A.C., Shevohenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Schmutz, J., Maring, M., Madan, A., Schmutz, J., Schmutz, 
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C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
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JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
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Pred. No. 4e-53;
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ADGKLSVKFGVLFQDDRCANLFBALVGTLKAAKRRKIVTYAGELLLQGVHDDVDIVLL
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                                                                                                                                                                                                                                     Direct Submission
Submitted (12-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
Tissue Procurement: Marcello Bento Soares, Ph.D.
Tissue Procurement: Marcello Bento Soares, University of Iowa
CDNA Library Arrayed by: Bento Soares, University of Iowa
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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29.8%; Score 249.2; DB 10; Length 526;
cal Similarity 74.4%; Pred. No. 3.5e-46;
390; Conservative 0; Mismatches 108; Indels 26;
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/clone=ThAGE:1448067"
/ssue type="Mammary gland"
/clone_lib="coares_mammary_gland_NbMMG"
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Contact: MGC help desk
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'protein id="AAH39801.1"
'db_xref="G1:24980968"
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/Ancte="synonym: 1700028104Rik"
/db_xref="LocusID:73112"
/db_xref="MGI:1920362"
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/strain="C57BL/67"
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## ALIGNMENTS

nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of the breast, lung, prostate, ovary or colon. PSGen 13 may also be used to suppress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vascularisation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the coding sequence of human Progression Suppressed Gene 13 (HubSGen 13)

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                                                                                                                            1 GGCACGAGGCTTGAGGGCAGAACACTTACTTTTCCCCCTACCCTGCTCCTCCTCCTCCT
                                                                                                                                                                    1 GGCACGAGGCTTGAGCGCAGAACACTTATCTTTTCCCCTACCTGCTCCTCCTCCTCCA
                                                                                                                                                                                                                 CAGCCGTCTTTCTCTTTGCCTCAGCCACTTCCTTCGCTTCACCCTCACCCTCAGCAC
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                                                                                      0
                                       100.0%; Score 835; DB 6; Length 835; 100.0%; Pred. No. 9.6e-201; cive 0; Mismatches 0; Indels 0
Sequence 835 BP; 246 A; 160 C; 176 G; 253 T; 0 U; 0 Other;
                                     Query Match
Best Local Similarity 100."
Matches 835; Conservative
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The present invention relates to methods of diagnosing breast cancer in a patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867—
ABT1112, where a differential expression of the genes indicates breat cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a coreening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be the onset or progression of breast cancer. The breast cancer genes may be the onset or progression of breast cancer. The breast cancer genes may be called as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention. Note: The sequence data for this patent electronic format directly from WIPO at cleatronic format directly from WIPO at the prise of the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GAGGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing breast cancer in a patient comprises detecting the level ogene expression in cell or tissue samples, where a differential gene expression is indicative of breast cancer.
                                                                                                                                                                                                                                                       Human; breast specific gene; breast cancer; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                   Human breast cancer associated coding sequence SEQ ID NO: 948.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 948; 260pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                     cytostatic; gene therapy; gene; ss.
                              ABT10814 standard; cDNA; 653 BP
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25-APR-2001; 2001US-0286090P.
23-MAY-2001; 2001US-0292517P.
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                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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Matches
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The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, and propholy, and infective, gynescological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome flontification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens way be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, disorders, wounds, and infectious diseases. AAPI6506 to AAPI6514 to AABS7303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                Sequence 778 BP; 250 A; 151 C; 148 G; 221 T; 0 U; 8 Other;
                                                                                                                                                                                                    invention
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                                                                                                                                                                                                                                                                                                                                  353 AACTGGAATATAAAGTGAAAGAACAATTTGAACATACTTAATGTATTTTTTATAGAAC
                                                                                                                                                                                                                                       608 AATCTATGTATGATGCTATAAATAAATCCTATTATTTTTTCTCAGGAATCTGGTTAGGAA
                                                                                                                                                                                                                                                                                                          ACATITITCIATAGATATITIGACATTCTGCGAAAGCAACAAGCAAACTGAAGACCAACTCC
                                                                                                                                                                                                                                                                                                                                                                                                              113 ACATITITCIATAGATATITIGACATICTGCGAAAGCAACAAGCAAACTGAAGACCAACTCC
                               TTACTGCCAAGATTAATGTGGGTTTACATATCTTTATGTACTGCCATTTTTTTGTTTCTGGTA
                                                           488 AACTGGAATATAAAGTGAAAGAACAAACATTTGAACATACTTAATGTATTTTTATAGAAC
                                                                                                                                                                   TITGIAAACGAAAGGAGAITCAIGIITIIAGAAGICIGICCIITITIAIAICIIGAAAGAA
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 Length 778;
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74.2%; Score 619.4; DB 3; 99.8%; Pred. No. 2.7e-146; iive 0; Mismatches 1;
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   Query Match 74.2
Best Local Similarity 99.8
Matches 620; Conservative
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referred to as prostate cancer, and diagnosis of disorders

sequences, 1 prevention,

Prostate cancer associated gene antigens, useful for treatment,

Rosen CA, Ruben SM; WPI; 2000-587513/55. P-PSDB; AAB56907. such as prostate cancer.

AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.

Claim 1; Page 1004-1005; 2338pp; English.

388 516 448 576 508 636

GCAAGGTGTTCATGATGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATAT

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TITGAACATACITAATGTATITITTATAGAACTITGTAAACGAAAGGAAGATICATGTITA

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AGGAACTCTTAAAGCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCT

3397 3397 329 339 339 517 509

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The invention relates to the isolation of genes AAC66410-C66458 encoding 49 human secreted proteins AAB32002-B32050. The genes can be used to generate fusion proteins by linking to the genes can be used to immunoglobulin G Fc portion (SECDID) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, amelicating or treating medical conditions, e.g. by protein or gene therapy. The genes and soldered from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antipagonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, (c) cardiovascular disorders such as myocardial isohaemias, (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156
                                  antiallergic; hepatofropic; antidiabefic; antilnflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antimugal; antiparaatic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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neuroprotective; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 336; 423pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0126596P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2000; 2000WO-US007483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602357/57.
P-PSDB; AAB32005.
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                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
22-DEC-1999;
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colon cancer polypeptides and polynucleotides, useful as vaccines, diagnosing, preventing, and treating colon cancer, and as markers for progression of cancer.
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                                                                    816
  969
                                                                                                                                                                                                                               Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
                                   597 GGGATGGGAATGTTTGTTCATAATTAATTAGACATTTTCTATAGATATTTGACATTCTGC
                                              GABAGCAACAAGCAAACTGAAGACCAACTCCTATGAGAAATATTATGATGTTTATGTAAT
  CTATTATTTTTCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCA
                                                                   GAAAGCAACAAGCAAACTGAAGACCAACTCCTATGAGAAATATTATGATTTATGTAAT
                                                                                                                                                                                                               SEQ ID No 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ID NO 939; 147pp; English
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                                                                                                                                                                                                                colon tumour protein,
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                                                                                                                                                   AAAGACATGTAACTGTCTT
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genetic analysis; diagnostic; antisense therapy; gene;

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The invention relates to polymucleotides encoding colon tumour proteins. The polymucleotides and encoded polypeptides are useful in pharmaceutical compositions, such as vaccines, for the diagnosis, prevention, and treatment of colon cancer. Polymucleotide sequences may be used as hybridistation probes or primers, and in the design and preparation of proteins in tumour cells. The compositions are useful for stimulating and immune response against cancer, particularly for the immunchheapy of colon cancer, and as markers for the particularly for the immunchheapy of himen cancer, and as markers for the progression of cancer. ABX4450-ABX46237 represent coding sequences of human colon tumour proteins of the invention. Note: with the exception of SEQ ID No 1 and 2, the sequence data for this parent did not form part of the printed specification but was supplied by the European Patent Office
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Sequence 552 BP; 190 A; 104 C; 75 G; 183 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                   GATGATGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGC 373
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                                                                                                                         Greeterreargaraargreeaacterrraaagearregraegaacterraaa
                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGTCTGTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGITICATAAATAATTAGACAITITICTATAGATAITIGACAITCTGCGAAAGCAACAAGC
                                                                                        290 GTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAA
                                                                                                                                                                                                                                                                                                                                              CATTITITIGITITCIGGIAAACIGGAATAIAAAGIGAAAGAACAAACATITGAACAIACITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGTATTTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGCCTGTCCTT
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                                                                                                                                                                           GCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGGCTGCTTCTGCAAGGTGTTCAT
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                                                                                                                                                                                                                  492 GCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCAT
                                                                                                                                                                                                                                                            GATGATGTTGACATTATATACTGCAAGATTAATGTGGTTTTACATATCTTTATGTACTGC
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    Length
                                               Indels
65.0%; Score 542.8; DB 6;
99.6%; Pred. No. 5.2e-127;
live 0; Mismatches 2;
  Nuery Match
Sest Local Similarity 99.6
Aatches 544; Conservative
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forensic; mapping; Human colon cancer related nucleotide sequence SEQ ID NO:750. Human; colon cancer; cancer; tissue profiling; Q57055 ABQ57055 standard; cDNA; 594 BP. 02-AUG-2002

366

expressed in cancer tissues. ABB78993 to ABB79004 represent proteins expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABG60776 to ABB60787 uncleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymuleotide amoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), a useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence of colon cancer in a cell or tissue type, for determining the presence of state of other type of cancer, in antisense therapy, to generate macroarrays on a soild surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensics, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists 367 125 187 365 AGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATTA 425 New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell tissue type, and in antisense therapy. GICTITCICITITGCCTCAGCCACTICCTTCGTTCGCCTCACCCCCCAGTGCACTGAAG 68 gretricierriscercadecaerrecrieerresecteaectececeaerseag 128 AAGGIAACCGGGICCAGACCCACGCGGCGCCAGIICTCCCGGCGGGGAAGGAAAACCGCGCA 188 GAGAGGCAGCAATGATGAGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTT TGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTTCCGTGATG ATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGA ATABATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGA 6 GAGGCTTGAGCGCAGAAACACTTACTTTTCCCCCTACCCTGCTCCTCCTCCTCCACAGCC GGGTCTTGAGGGGAGAAAAACTTACTTTCCCCCTACCCTGCTGCTCCTCCTCCTCCTCAACACACAGCC GAGAGGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTT Gaps Molino GA 0 Length 594; Sequence 594 BP; 157 A; 142 C; 134 G; 149 T; 0 U; 12 Other; Dwivedi P, Indels 74; DB 6; 53.9%; Score 450.2; DB 6 86.8%; Pred. No. 1.3e-103 Catino TJ, 0; Mismatches Burgess C, Astle JH, Carroll E, Thiaglingam A, Lewis ME; Claim 1; Fig 1; 796pp; English 02-OCT-2000; 2000US-0237271P. 02-OCT-2001; 2001WO-US030732 Query Match Best Local Similarity 86.8 Matches 488; Conservative WPI; 2002-426115/45. (FARB ) BAYER CORP. WO200229086-A2 Homo sapiens. 11-APR-2002 186 246 œ 99 248 306 308 ò g g à g ઠ 셤 ે 임 à 쉱 ઠે

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127 185

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245 247 305 Gaps ..

8; Indels

0; Mismatches

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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB7893 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 mucleic acid sequences. (I) can be used in antisherse therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polymucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived furm (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of clans from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forenside, canalysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
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                                                                                                                                                                                                                                                                                                                                           488 AATACTTGGNCCACGGAACAAGGTANCCTAGGGATAACAACGCAATNCTNTTTNTNAAAG 547
486 TAAACTGGAATATAAAGTGAAAGAACAAACATTTGAACATACTTAATGTATTTTTATAGA 545
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                                                                                                                         TATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTTGTTTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; cancer; tissue profiling; forensic; mapping; genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer related nucleotide sequence SEQ ID NO:748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 TCCATATTAACAATANGGGTTT 569
                                                                                                                                                                                                                                                                                                                                                                                                                                546 ACTITGIAAACGAAAGGAGATT 567
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Thiaglingam A, Lewis ME;
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52.3%; Score 436.8; DB 6; Length 717; 97.8%; Pred. No. 3.4e-100;

Query Match Best Local Similarity

Sequence 717 BP; 192 A; 171 C; 155 G; 180 T; 0 U; 19 Other;

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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver
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                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
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                                                                                                                                                                                                                                                                   251 İGGGİTCAAAAATGCIGAIGGAAAĞITAAGCGİGAAATITIGGGGICCTICCGIGAIG
                                                                                                                                                                                                                                                                                               306 ATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGA
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                                                                                                                                                                                                                                                                                                                        311 ATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGGTGCAAAACGAAGGA
                      GAGGCTTGAGCGCAGAAACACTTATCCCCCCTACCTGCTCCTCCTCCTCCACAGCC
                                      11 GGGTCTTGAGGGGAGAAACACTTACTTTTCCCCTACCTGCTCCTCCTCCTCCTCCTCCACAGCC
                                                                            GICITICICITIGCCICAGCCACTICCTICGCCICACCCICCCCAGTGCACTGAAG
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                                                                                                                                                                                                     246 TGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     431 TATTACTGCAAAGAATAAATGNGGGTTACATATCTTTATGTAC 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peres-Da-Silva S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene #687 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN94189 standard; DNA; 406
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453; Conservative
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tumour in a patient, and differentiating metastatic liver cancer from expression of two or more genes represented in ABN93503-ABN9455 in a tissue sample. The method of the invention has hepatotropic, and tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism. Note: The sequence data for this patent did not form part of the printed specification, but was fitp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 eeecaeeeareeaarerrrerrearaaraarraeacarrrreraraeararrreear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 406 BP; 140 A; 68 C; 48 G; 150 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uery Match 45.8%; Score 382.4; DB 6 lest Local Similarity 99.7%; Pred. No. 1.5e-86; latches 383; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812 GTAATAAAGACATGTAACTGTCTT 835
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20-FEB-2001; 2001US-0270216P.
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ABL38512 standard; cDNA; 368
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blood vessel; nasopharyngeal tumour; thyroid tumour; leukaemia; lymphoma;
breast; lung; prostate; ovary; colon; gene; ss.
                                                                                                                                                      ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour
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                                                                       Novel isolated colon tumor polynucleotide differentially expressed colon tumor or colon metastatic tumor and polypeptides encoded by tuseful for inhibiting development of cancer in patient.
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                                                                                                                                                                                                                                                                                                                            DB 6; Length 368;
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                                                                                                                                                                                                                                                                                                Sequence 368 BP; 128 A; 65 C; 44 G; 128 T; 0 U; 3 Other;
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                                                                                                                                                                                                                                                                                                                            Query Match
43.7%; Score 365.2; DB 6;
Best Local Similarity 99.2%; Pred. No. 3.2e-82;
Matches 365; Conservative 1; Mismatches 2;
                                                                                                                                    Claim 1; SEQ ID NO 2101; 105pp; English.
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                                                  WPI; 2002-114514/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel isolated nucleic acids which encode a rat or human Progression Suppressed Gene 13 (PSGen 13) protein. The nucleic acids are useful for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer, e.g. nasopharyngeal tumour, thyroid tumour, leukaemia, lymphoma, or cancer of tupbress the transformed phenotype of a malignant cell. Administration of PSGen 13 gene or protein may result in a decrease in tumour mass, number of cancer cells, serum tumour marker, tumour metastasis, vasculariation, perfusion, or rate of tumour growth, improved clinical symptoms, and/or increased patient survival. The present sequence represents the coding sequence of rat Progression Suppressed Gene 13 (rPSGen 13)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 TCACCCTCCCCAGTGCACTGAAGAAAGGTAACCGGGTCCAGACCCACGCGGCGCCAGTTCT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 TCTTAAAGCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGGCTGCTTCTGCAAGG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTCATGATGATGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTAT 462
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                                                                                                                                                                                                                                                                                                                                                                   New rat and human Progression Suppressed Gene 13 for preventing the growth of cancer cells and/or new blood vessels, and for treating patients suffering from a cancer.
                                        /*tag= a
'product= "Progression suppressed gene 13 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 218; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.1%; Score 335.2; DB 6 69.1%; Pred. No. 1.6e-74;
Location/Qualifiers
                                                                                                                                                                                                                                          (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 1; 53pp; English.
                                                                                                                                                                                                        25-AUG-2000; 2000US-00648310.
                                                                                                                                                                   27-AUG-2001; 2001WO-US026795
                    170. .415
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                                                                                                                                                                                                                                                                                                                   WPI; 2002-280914/32.
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Best Local S
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761
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                                                                                                                                                                                                           478 AAGTTCCTTATGTATTTTATAGACCTTTGTAAACAAAAGGGGA--CTTGTTGAGAAGTC 535
                                                                                                                                                                                                                                                                                                                                                 536 CTGTTTTTATACCTTGGAGCAAAACATTACAATGTAAAAATAAACAAAACCTGTTATTTT 595
                                                                                                                                                                                                                                                                                                                                                                                                                         642 ATTTTTCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCAGGGAT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          596 TTTTTTCTTAAGAAGGTAATCGGGAGACGTAGGGCAATAAAATGTTTTCAGAGGTGCGAAA 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 656 AAGCTTTTGTTTTCTTAAACCATTCTTAGTCT--CTGCCACACTTGACACTCCGTCAAAG 713
                                                                    436 GTA------TCTGGTAAACTGGAATAATTAAGTTAAGGAGACAAACAT---G 477
                                                                                                                                         522 ACATACTTAATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGT 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         762 CAACAAGCAAACTGAAGACCAACTCCTATGAGAAATATTATGATGTTTATGTAATAAAGA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              714 TGAGAAGCGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTTATGTAATAAAAAAA 773
GTACTGCCATTTTTTGTTTCTGGTAAACTGGAAT-ATAAAGTGAAAGAACAAACATTTGA 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumor progression.
                                                                                                                                                                                                                                                                               702 GGGAATGTTTGTTCATAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Progression suppressed gene, PSGen, progression elevated gene, PEGen, tumour, reciprocal subtraction differential RNA display, RSDD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "PSGen13"
/note= "Progression suppressed gene 13 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differential expression; gene cloning; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Progression suppressed gene 13 (PSGenl3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
170. 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ21517 standard; cDNA; 800 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCO ) UNIV COLUMBIA NEW YORK.
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P-PSDB; AAY39325.
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774 AA 775

subtraction differential RNA display (RSDD) between the two samples to generate two subtraction samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed. The method is used to identify and clone differentially expressed genes, particularly those with increased or reduced expression during tumour cell progression, e.g. progression suppressed or progression and progression elevated genes (PEGen). The method reduces the complexity (where bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated, allowing identification and cloning of genes displaying anticipated differential expression. RSDD requires only a single anchored primer for amplification and reamplified CDNA can be analysed by reverse Northern blotting

Sequence 800 BP; 243 A; 153 C; 185 G; 219 T; 0 U; 0 Other;

103 TCACCCTCCCCAGTGCACTGAAGAAGGTAACCGGGTCCAGACCCCACGCGGCGCCAGTTCT 162 76 rerrecreterrades de cesas de creasers de casacidades de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias d CITAGIGGAGGAAATICAICGITIGGGITCAAAAAIGCIGAIGGAAAGITAAGCGIGAA 282 255 341 256 GTTTGGGGTCCTCTTCCAAGACGACAGATGTGCCAATCTCTTTGAAACCGTTGGTGGGAA 315 400 401 GGTGTTCATGATGATGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTT 460 376 GGTGTTCATGATGATGTTGACATTGTATTGCTGCAAGATTAATGTGGGTTTGCAGATCTGG 435 436 GGGTA------TCTGGTAAACTGGAATAATTAAGTTAAAGGAAAAAAH 520 GAACATACTTAATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAA 579 536 TCCTGTTTTTATACCTTGGAGGAAACATTACAATGTAAAAATAAACAAAACTGTTATT 595 TIAITITICICAGGAAICIGGITAGGAATIGCAGGCAAIGAGATITITIGCGGGGCAGGG 699 irriririritzinakakagararicakakakakarararararariri engakakakaka 655 700 ATGGGAATGTTTGTTCATAAATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAA 759 713 714 AGTGAGAAGGGAACTAAAGACCAACTGCGGTGGAAAATATTATGTTATGTAATAAAAA 773 75 479 -GAAGITCCTTATGTATTTTTATAGACCTTTGTAAACAAAAGGGGA--CTTGTTGAGAAG 16 derecerecerrerecacrecarecerrirererrascesascesarerrerrace 136 TTCAGTGAAGAAGGAATCGGAGGGTCAGGAATGAACGTGGAGCATGAGGTTAACCT censeries as de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra de la contra della ATTTGGGGTCCTCTTCCGTGATGATAATGTGCCAACCTCTTTG-AAGCATTGGTAGGAA CTCTTAAAG-CTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAA crergaaagecegeaaaagaagaargaracgraegaagagagecrerrregaa 461 AIGTACTGCCATTTTTTTTTTTTCTGGTAAACTGGAAT-ATAAAGTGAAAGAACAAACATTT 656 AAAAGCTTTTGTTTTCTTAAACCATTCTTAGTCT--CTGCCACACTTGACACTCGTCAA AGCAACAAGCAAACTGAAGACCAACTCCTATGAGAAATATTATGATATTATGTAATAA uery Match 37.1%; Score 310; DB 2; Length 800; est Local Similarity 68.7%; Pred. No. 3.8e-68; atches 537; Conservative 0; Mismatches 220; Indels 25; Gaps GA 821 223 196 342 596 316 640 820

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are darived from RNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                  numan; 5' {\tt EST}_i expressed sequence tag; secreted protein; {\tt cDNA} isolation; gene therapy; {\tt chromosome} mapping; {\tt ss}_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487 AAACTGGAATATAAAGTGAAAGAACAAACATTTGAACATACTTAATGTATTTTTATAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAACTGGAATATAAAGTGAAAGAACAACATTTGAACATACTTAATGTATTTTTTATAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATCTATGTATGATGCTATAAAATAAATCCTATTATTTTTTCTCAGGAATCTGGTTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a S' expressed sequence tag (S' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 34272; 71pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 296 BP; 105 A; 32 C; 57 G; 100 T; 0 U; 2 Other;
                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 34272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 33.5%; Score 279.6; DB 3. Local Similarity 99.3%; Pred. No. 1.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                        Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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AAC30197 standard; cDNA; 296 BP.
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                                                                       (first entry)
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                                                                       06-OCT-2000
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                                     AAC30197;
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New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; colon cancer; cancer; tissue profiling; forensic; mapping; genetic analysis; diagnostic; antisense therapy; gene; ss.
                                                                          GACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAGCAAACTGAAG 778
                                                                                                          33.5%; Score 279.4; DB 6; Length 627;
ilarity 76.9%; Pred. No. 1.8e-60;
Conservative 0; Mismatches 19; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                   related nucleotide sequence SEQ ID NO:557
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Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2000; 2000US-0237271P
                                                                                                                                                                                                                                                         ABQ56862 standard; cDNA; 627
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
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les 429; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer
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Matches
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19 AGAAACACTTACTTTTCCCCCTACCCTGCTCCTCCTCCACAGCGG--TCTTTCTCTT 559 AGAACATTACTTTTTTCCCCTTACCTGGTCTTCTTCTCCTCCACAGCNGTTTTTTTTT TOCCICAGCCAC-TICCTICGTICGCCICACCCCCCAGGCACGAAGAAAGAAACG 138

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New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                            268
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199 IGCCTCAGCCACTTTCCTTCGCCTCACCCTCCCCAGTGCATTGAAGAAGGTAACCG 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                             199 AAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAA
                                                                                                                                                                                                                                                                                                                                                                 389 CTGCTTCTGCAAGGTGTTCATGATGATGTTGACATTATATATGTGGT
                                                                                                                                                                                                                                                     269 AAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTGAA
                                                                                                                                                                                                                                                                                                           329 GCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAG
                                                                                                                                                                                                                                                                                                                                    139 GCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGAAGATTGTAACATATCCAGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                 79 CIGCTICTGCAAGGIGTICATGAIGAIGTIGACATIATAITACIGCAAGAITAATGIGGI
                                                                                                           379 CATCTGCCTTTAGAATGTGAGATCCCCGAGGGCAGATCCTGTGCTACACACCTTTTGTAT
                                                                                                                                         190 -----GGCAGCAATGAATGTGGAT
                                                                                                                                                                   209 CACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAAAATGCTGATGGA
                                                                                                                                                                                                              Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stache-Crain B, Dickson MC,
                                GGTCCAGACCCACGCGCGCCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                          449 TIACATATCTTTATGTAC 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACH38863 standard; cDNA; 458
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STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DRMA) DRMANAC R T
(LABA/) LABAT I.
(STAC/) STACHE-CRAII
(DICK/) DICKSON M C
(JONE/) JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003073623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH1789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purlified polyneptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in formalics, in assessing bloidiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful disorders and other traits. The nucleotide for contingent manufacturing the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense by sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antibifiammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianemic; antiarthritic; cancer; antifreumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 GGTTCAAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGAT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 GAGGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGAAATTCATCGTTTG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 gadgcagcaangaangnggancacgaggnaacchcriagiggaggaaanrcarcgriig 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 GGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATIGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATT 458
                                                                                                                                                                                                                                                                                                                                                                                                          Length 458;
                                                                                                                                                                                                                                                                                                                                                                      Sequence 458 BP; 112 A; 86 C; 149 G; 107 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human nervous system related polynucleotide SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                        28.4%; Score 237; DB 8; L
100.0%; Pred. No. 8.4e-50;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  seqdata.uspto.gov/sequence.html?DocID=20030073623
Claim 1; SEQ ID NO 26075; 44pp; English.
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ABAll066 standard; cDNA; 351 BP
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; 2000US-0180628P.
; 2000US-0184664P.
; 2000US-0186350P.
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 237; Conservative
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24-FEB-2000;
02-MAR-2000;
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20000G 0231414P
20000G 02319BP
20000G 02319BP
20000G 023239BP
20000G 023239BP
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The invention relates to novel genes (ABAl1004-ABA21534) and proteins (ABBA678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and orbar cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune bracet, gastroinmente thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthrifis and ulcerative collitis, (c) multiple sclerosis, rheumatoid arthrifis and ulcerative collitis, (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections, Note: The sequence data for this patent did not form part the printed specification, but was obtained in electronic format directly the WIPO at ftp.wipo.int/pub/published\_pot\_sequences

Sequence 351 BP; 104 A; 72 C; 103 G; 72 T; 0 U; 0 Other;

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20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-024186P.
20-OCT-2000; 2000US-024186P.
20-OCT-2000; 2000US-024186P.
20-OCT-2000; 2000US-024481P.
20-OCT-2000; 2000US-024461P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-024653P.
08-NOV-2000; 2000US-024653P.
08-NOV-2000; 2000US-024653P.
08-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024921P.
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Ruben SM (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC, WPI; 2001-541565/60. P-PSDB; ABB14740.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Claim 1; SEQ ID NO 73; 1701pp + Sequence Listing; English

114 AGTGCACTGAAGAAGGTAACCGGGTCCAGGCGCGCGGCGCCAGTTCTCCGGCGGAAG 173 90 Adrigeacridaadaaadaraaccdddreeacdeacdeacdecddearrereedddaad 149 210 AAATTCATCGTTTGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTTC 269 292 CCICTICCGIGALGARAATGIGCCAACCICTTIGAAGCATIGGIAGGAACICTIAAAGC 351 270 crenircegicardaraareree-acererirgaagea-regradgaaceerraaage 327 GAAAACCGCGCAGAGAGGCAACGAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGG 233 150 GAAAACCGCGCAGAGAGGCAACAATGAATGTGGGATCACGAGGTTAACCTCTTAGTGGAGG 234 AAATTCATCGTTTGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGT--Gaps 4; Query Match
25.9%; Score 216.4; DB 5; Length 351;
Best Local Similarity 96.2%; Pred. No. 1.2e-44;
Matches 254; Conservative 0; Mismatches 6; Indels 4; 352 IGCAAAACGAAGGAAGAIIGIAAC 375 328 ridcahahcdahddahdrirahc 351 174 g ò à 8

Search completed: March 17, 2004, 12:34:42 Job time : 445 secs

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Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metheria; Primates; Catarrhini; Hominidae; Homo.

Bukaryota; Matheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 845)

Stan, H. Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z.

I Unpublished

E (bases 1 to 845)

S Ye,M., Zhang, Q.H., Zhou, J., Shen, Y., Wu, X.Y., Guan, Z.Q., Wang, L.,

Fan, H. Y., Mao, Y.F., Dai, M., Huang, Q.H., Chen, S.J. and Chen, Z.

Direct Submission

L Submitted (14-MAY-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road II, Shanghai 200025, P. R. China

Location/Qualifiers
HTC 22-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens HSPC280 mRNA, partial cds. AF161398 GI:6841209 HTC.
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/mol_type="mRNA"
      Homo sapiens (human)
Homo sapiens
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
REFERENCE
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
AF161398
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AF116682 Homo sapi
BU849360 AGENCOURT
BI859694 603386283
                                                                                                          March 17, 2004, 12:23:02; Search time 2821 Seconds (without alignments) 8839.036 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                          1 (bases 1 to 876)
Zhang, C., Yu, Y., Zhang, S., Wei, H., Zhou, G., Ouyang, S., Luo, L.,
Bi, J., Liu, M. and He, F.
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// Mol type="mRNA"
/ Mb xref="taxon:9606"
/ clone="INABE:5697818"
/ lab_host="INABE:5697818"
/ lab_host="DH10B (T1-phage-resistant)"
/ clone=lbb="WhH MGC 128"
/ none=lbb="WhH MGC 128"
/ note="Wetcor: pDNH-LiBs is lie 1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgcctcggcc); Double stranded cDNA was prepared from a pool of 40 cell line pol/A+ RNB (bladder 2 blood 3 3 4 k) brain - 5.6 k) breast - 12.5 k, colon - 4 connective tissue - 1.4 k, eye - 1 k, intestine - 2.6 k, kidney - 2.2 k, liver - 5.7 k, lung - 10.8 k, NK-cell - 5.2 k, ovary - 4 k) pharynx - 2.5 k, prostate - 4.3 k, salivary gland - 1.3 k, and skin - 2.3 k) s and 3 k adaptors were used in cloning as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 16-OCT-2002
426 AAACTGGAATATAAAGTGAAAGAACAACATTTGAACATACTTAATGTATTTTTATAGAA 485
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                                                                                                     AAACTGGAATATAAAGTGAAAGAACAATTTGAACATACTTAATGTATTTTTATAGAA 546
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 816)
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Thissue Procurement: NCI
Thissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayd by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
This is a consortium to the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consortium of the consorti
                                                                                                                                                                                                                                  CTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGTCTGTCCTTTTTTATATCTTGAAAGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCOURT 10432847 NIH MGC_128 Homo sapiens cDNA clone IMAGE:6597818 5', mRNA sequence.
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/organism="Homo sapiens"
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797 bp mRNA linear EST 10-OCT-2001
803386283F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5394836 5',
B1859694
                     5'-ATTCTAGAGGCCGAGATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >2 kb size fraction (chher fractions present in NIH MGC 122). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH MGC
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                                                                                                                                                                                                                                                                                89.9%; Score 750.6; DB 13; Length 816;
99.3%; Pred. No. 2e-168;
iive 0; Mismatches 4; Indels 1; Gaps
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
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Best Local Similarity 99.34
Matches 764; Conservative
                                                                                                                                                                                             Library."
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AAGTGAAAGAACAAACATTTGAACATACTTAATGTATTTTTTTATAGAACTTTGTAAACGAA
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Homo sapiens
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                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

B. (Loases I to 797)
E. (Loases I to 797)
E. (Loases I to 797)
L. Orpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Lloadion/Qualifiers
High quality sequence stop: 787.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="none Saptens"
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//do xref="taxon:9606"
//done="lype="mrm."
//done="lype="mrm."
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//done="lorgan: Breast; Vector: pCMV-SPORT6; Site_1: Not1;
//note="lorgan: Breast; Vector: pCMV-SPORT6; Site_1: Not1;
//site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 &b. Library enriched for full length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Pred. No. 3.5e-165;
O; Mismatches 15;
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/organism="Homo sapiens"
              BI859694.1 GI:16000441
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ilarity 97.7%;
Conservative
                                                Homo sapiens (human)
                                                                      Homo sapiens
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/organism="Homo sapiens"
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/db_zref="txxon:9506"
/db_zref="txxon:9506"
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/done="organ: Left Pubic Bone; Vector: pT7T3-Pac
/done="organ: Left Pubic Bone; Vector: pT7T3-Pac
/done="organ: Left Pubic Bone; Vector: pT7T3-Pac
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containing the following tissue (8): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
line CS5. The library was constructed according to
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UI-H-ED1-axw-a-08-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5834383 3', mRNA sequence.
BQ015110
EQ015110.1 GI:19740011
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Email: cgapbs.r@mail.nih.gov
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Edguencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be
Clone Distribution: Clone distribution information can be
through the I.M.A.G.E. Consortium/Libla at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
Seq primer: Mi3 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 GAGATITITIGCGGGGGAGGGAATGGGAATGTTCGTTCGTAACATAATTAGACATTTTCTA 719
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1 (bases 1 to 749)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
480 AAGIGAAAGAACAAACAITIGAACAIACIIAAIGIAITITITAIAGAACIIGGIAAAACGAA
                                                                                                                                                                                            600 AIGCIAIAAAAIAAAICCIAIIAIIIIITICICAGGAAICIGGIIAGGAAITIGCAGGCAAI
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                                                                                                                            560 AGGAGATICATGITITAGAAGICTGICCTITI
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I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT. TAG_TISSUE-chondrosarcoma TAG_LIB=UI-H_DI TAG_SEQ=CGTCAAGGCT."
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                                                                                                                                                                                                                                                                                                                                                                                                          689 AAGGAAAACCGCGCAGAGGGAGCAATGAATGTGAATCACGAGGTTAACCTCTTAGTGG
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                                                                                                                                                                                                      uery Match 85.7%; Score 715.6; DB 12; Length 749; est Local Similarity 99.0%; Pred. No. 4.4e-160; atches 718; Conservative 0; Mismatches 7; Indels 0;
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AV717724 DCB Homo sapiens cDNA clone DCBBED06 5', mRNA sequence. AV717724

AV717724.1 GI:10814876

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 GAGAGGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 TGGGTTCAAAAAATGCTGATGGAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 IGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTTGGGGTCCTCTTCCGTGATG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 ATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 ATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACGAAGGA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 AGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATTA 425
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                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 741)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Lu,G., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Homo sapiens Cabha DCB clones
Unpublished (2000)
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Chinese National Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol type="mRNA"
/db_xef="texxon:960s"
/clone="pcbsxon:960s"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="amst.ws"
/lab_host="bcbs"
/clone=lib="bcs"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
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Homo sapiens (human)
Homo sapiens
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AV713584 Innear EST 11-OCT-2000 AV713584 DCB Homo sapiens CDNA clone DCBBBB10 5', mRNA sequence.
241 CAAAACGAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATG 300
                                                                                                                           301 ArgrīdaČAltAlArtaCidCAAGALTAArGidGTTTACATATCTTVAGTACTGCCATT 360
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(bases 1 to 714)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,O., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Liu,G., Cheng,Z., and Han,Z.

Un,G., Cheng,Z., and Han,Z.

Unpublished (2000)
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Contact: Zequang Han
Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzgedeng.sh.cn
This clone is available at CHGC in Shanghai.
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/note="Vector: pTriplEx2; Site_l: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                 654 AATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCAGGGATGGGAATGTTTGT
                                                                                                                                                                                                                                                                                  534 IATTITIATAGAACTITGTAAACGAAAGGAGAITCATGTITTAGAAGTCTGTCCTTTTTT
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/db_xref="taxon:9606"
/clone="DCBBBB10"
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/lab_host="BM25.8"
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                                                                                                  726 AGACATITICTATAGATATITGACATICTGCGAAAGCAACAAGCAAACTGAAGACCAACT 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 GAAAACCGCGCAGAGGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGG 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherita; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 752)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Chong,Z., Xu,X., Xu,X., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,Y., Gu,Y., Yu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Liu,G., Cheng,Z., and Han,Z., Jia,J., Fu,G., Ren,S., Zhong,M., Homo sapiens CDNA DCB clones
Unpublished (2000)
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Chinese National Human Genome Center at Shanghai
315 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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  666 AATTGCAGGCAATGAGATTTTTTGCGGGCCAGGGATGGTGGTTTTTTTAATAATT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBARC08"
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lab_host="BM25.8"
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1 (bases 1 to 90; 1)

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                           Length 714;
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                           DB 9;
                           Score 683.8; DB 9;
Pred. No. 1.7e-152;
0; Mismatches 9;
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National Cancer Institute / NIH
Bldg. 31 Rm10Ao7 Bethesda, MD 20892
Email: Gagaba-Kemail..iih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM209 row: a column: 24
High quality sequence stop: 543.
High quality sequence stop: 543.
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Pred. No. 4.4e-150;
0; Mismatches 27; Indels 3;
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// nol_type="mRNX"
// db_xref=txxxn:9666"
// db_xref=txxxn:9666"
// db_vref=txxxn:9666"
// dav_stage="8-9 weeks"
// dav_bet="bl108"
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BX110370 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGp998B181944<sup>7</sup>; IMAGE:788657, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 676)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Human UnigeneSet - RZPD3

Unpublished (2003)
                                                                                                                                      TIGAAAGAAAATCTATGTATGATGCTATAAATAAATCAATTATTTTTCTCAGAATCT
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RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Nueuchieimer Feld 580, D-69120 Heidelberg, Germany
RZDD; IMAGD998B18944*
RZPDLIB, I.M.A.G.E. cDNA Clone Collection;
Human Unigenedet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.de/CloneCards/cgi-
http://www.rzpd.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
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SFERENCE AUTHORS

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TITLE JOURNAL DMMENT

EATURES

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717 bp mRNA linear EST 20-SEP-2002
_BB22409 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6457680
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1 (bases 1 to 717)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                          1 creaacaaaceraaceeeerceacaceececeeececeacriciceeeceeeaaace
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DB 13; Length 676;
                                               Indels
  Score 671.4; DB 13
Pred. No. 1.6e-149;
0; Mismatches 4;
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Tissue Procurement: NCI
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AGENCOURT B822409 NIH_MGC
5', mRNA Sequence.
BUS98760 I GI:23250519
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Homo sapiens
  Query Match 80.4%;
Best Local Similarity 99.4%;
Matches 672; Conservative
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481 TICTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCAGGGATGGGA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ACTGGAGGAAATTCATCGTTTGGGTTCAAAAAATGCTGATGGAAAGTTAAGCGTGAAATT
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         cDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M. 4G.E. Consortium (LLNL) CONA Sequencing by: The I.M. 4G.E. Consortium (LLNL) CLOR distribution: MGC clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCM2639 row: p column: 01 Plate: LLCM2639 row: p column: 01 High quality sequence stop: 655.
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IGIN

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/oreganism="Homo sapiens"
// mol_type="mRNA"
// mol_type="mRNA"
// db_tyfe="mRNA"
// clone="type="embryonal carcinoma"
// issue_type="embryonal // issue_type="emb
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                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapba-r@mail.nih.gov
Tissue Procurement: Array
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCMA527 row: p column: 02
High quality sequence stop: 734.
Location/Qualifiers
                                                                                             541 AIGITIGITICATAAATAATTAGACATTITICTATAGATATTIGACATTCTGCGAAAGCAAC 600
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                                                                                                                                                                                                            766 AAGCAAACTGAAGACCAACTCCTATGAGAAATATTATGATGTTTATGTATAAGACATG
ATGTTTGTTCATAAATAATTAGACATTTTCTATAGATATTTTGACATTCTGCGAAAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
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239 299 419 121 181 241 300 GIGAIGAIAAAIGIGCCAACCICTITGAAGCAITGGIAGGAACTCTIAAAGCTGCAAAAC 359 242 drdardarahargroccaaccrorridaadcarrograccaacrorrahadcoroccaaaac 301 361 479 420 539 480 599 540 629 900 GITAGG-AATIGCAGGCAAIGAGAITITITIGCGGGCAGGGAIGGGAAIGITIGITCAIA 718 601 GITAGGAAATIGCAGGCAATGAGATTTTTTTTTTGCGGGGCAGGCATGGGAATGTTGTTCATA 660 ACTAATTAGACCATTTCTATAGATATTTGACATTCT--GGAAGGCACAAGCAAACTGAAG 718 CGCGCAGAGAGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAAAAATTC 240 ATCGTTTGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCC 182 Arcerriggerreaaaarecreareeaaaerraaecereaaarriggegereeree 360 GAAGGAAGATIGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTG 302 GAAGGAAGATTGTAACATATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTG ACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTGT 362 ACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCA-TTTTTGT 421 TTCTGGTAAACTGGAATATACAGTGAAAGAACAAACATTTGAACATAACTTAATGTATTTT 540 TATAGAACTITGTAAACGAAAGGAGAITCAIGITTTAGAAGTCTGTCCTTTTTATATCT 719 AATAATTAGACATTTTCTATAGATATTTGACATTCTGCGAAAGCAACAAGCAAACTGAAG TTCTGGTAAACTGGAATATAAAGTGAAAGAACAAACATTTGAACATACCTTAATGTATTTT 779 ACCAA 783 719 ACCAA 723 180 420 480 009 099 120

Query Match

765 bp mRNA linear EST 21-OCT-2002 IMAGE:6724487 5', mRNA sequence. SFINITION SULT 13 1953438

BU953438.1 GI:24183010 Homo sapiens (human) Homo sapiens ERSION EYWORDS DURCE ORGANISM CESSION

AUTHORS TITLE JOURNAL DMMENT SFERENCE

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 765)

S NIH MGC http://mes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: NCI

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioseience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

/Golding in the control of 40 RNAs) "

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5'-ATTCTAACAGCCGACATGGCCATTAGGCCGGG-3' Evll-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH\_MGC\_127
and NIH MGC\_128). Library created in the laboratory of Tusdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC http://image.llnl.gov Plate: LLCM9039 row: 1 column: 22 High quality sequence stop: 451. Location/Qualifiers /organism="Homo sapiens" FEATURES ORIGIN

115 GTGCACTGAAGGTAACCGGGTCCAGACCCACGCGCGCCCAGTTCTCCGGCGGGAAGG 174 175 AAAACCGCGCGAGAGGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGA 234 62 AAAACCGCGCAGAGAGGCAGCAATGAATGTGGATCACGAGGTTAAACCTCTTAGTGGAGGA 121 294 181 354 241 414 474 2 GGGCACTGAAGAAGGTGAAACTGGGCTCCAGACCCACGGGGGGCGCCCAGTTCTCCGGCGGGGAAGG 61 242 AAAACGAAGGAAGATIGIAACATATCCAGGAGGCTGCTTCTGCAAGGTGTTCATGATGA 301 235 AATTCATCGTTTGGGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGGTCCT 182 CTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGC 355 AAAACGAAGGAAGATTGTAACATATCCAGGAGGTGCTTCTGCAAGGTGTTCATGATGA 302 IGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCAITT TGTTGACATTATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTT 122 AATTCATCGTTTGGGTTCAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCT 295 CTTCCGTGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGC ô ch 78.8%; Score 657.8; DB 13; Length 765; 1 Similarity 94.8%; Pred. No. 2.8e-146; 690; Conservative 0; Mismatches 37; Indels 0; 415 Local Best Loca. Matches ద ò δ 셤 ò DD 8 g 8

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|                      | 302 AAACGAAGGAAGATTGTAACATATCCAGGAGAGGTGCTTCTGCAAGSTGTGTATCATTTGTAACGATTAATGTGGTTTACATATCTTTATGTACGCATTTTTTAGGTTAATGTGGTTTAACATTATGTAGGTTTAATGTGGTTTAATGTGGTTTAATGTGGTTTAATGTGGTTTAATGTGGTTTAATGTGGTTTAATGTGGTATTTAATGTGGAATTTAATGTTAATGTAAATGTAATGTAATGTAATGTAAAATGTAAAAAA                                                                                                                                                                                                                     |                                                                                             | RESULT 15 BG744405 LOCUS BG744405 LOCUS BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG744405 BG74405 BG744405 BG74405 BG74405 BG744405 BG744405 BG74405 BG744405 BG744405 BG74405 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG74407 BG744107  BG744117 |----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 54<br>77<br>77<br>66 | ITION 602550569F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4658032 5 mRNA sequence.  BG502291 BG502291.1 GI:13463808 BG5 Homo sapiens (human) BMISM Homo sapiens (human) BUKARYOTA: Merazaa, Chordata; Craniata; Vertebrata; Buteleosto Mammaila; Eutheria; Primates; Catarrhini; Hominidae, Homo.  BNS III (bases 1 to 74) HORS NIH-MGC http://mgc.nci.nih.gov/. BNC High Institutes of Health, Mammalian Gene Collection (MGC) NAtional Institutes of Health, Mammalian Gene Collection (MGC) | AL Choubild Contact Email: Tissue CDNA CDNA CDNA CDNA CONA CONA CONA CONA CONA CONA CONA CO | /tissue_type="embryonal carcinoma" //lab host="Dath) By try phage-resistant)" //clone lib="NHHH MGC 61" //clone lib="NHH MGC 61" //clone lib adaptors were used in cloning as follows: 5' adaptor sequence: 5'-Acadeacacaracacara-dr(30)BN-3' //clone lib adaptors were used in cloning as follows: 5' //clone lib adaptors were used in cloning as follows: 5' //clone lib adaptors were used in cloning as follows: 5' //clone lib adaptors were used in cloning as follows: 6' //clone lib adaptors were used in cloning as contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech //clone library." //clone library." //clone library watch //clone library lib adaptor lib adaptor lib lib adaptor lib lib lib lib lib lib lib lib lib lib                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

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/cote="Organ: bLood; Vector: pOTB7; Site_1: XhoI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 TTCAGTGAAGAAGGAATCGAAGGACGTCAGCAATGAACGTGGAGCATGAGGTTAACCT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 ceregresakahreareareareresarresakahareesakaereakareakah 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 AITIGGGGTCCTCTTCCGTGATGATAAATGTGCCAACCTCTTTG-AAGCATTGGTAGGAA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 CTCTGAAAGCCCGCAAAACGAAGGAAGATGTTACGTACGCAGAAGAGCTGCTTTTGCAA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520 GAACATACTTAATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAA 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536 TCCTGTTTTTATACCTTGGAGCAAACATTACAATGTAAAATAAAATAAAAACCTGTTATT 595
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                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                    37.1%; Score 310; DB 4; Length 800; 68.7%; Pred. No. 7.1e-72; Live 0; Mismatches 220; Indels
PRIOR APPLICATION NUMBER: US 09/197, 889
PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 09/185,115
PRIOR FILING DATE: 1998-11-03
PRIOR FILING DATE: 1998-02-27
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PRECENT OF WINDOWS Version 4.0
SEQ ID NO 26
LENGTH: 800
                                                                                                                                                                                                                                                                                                                              Best Local Similation
Matches 537; Conservative
                                                                                                                                                                                                                                       ORGANISM: homo sapiens
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APPLICANT: Fisher, Paul B.
TITLE OF INVENTION: Reciprocal Subtraction Differential
TITLE OF INVENTION: Display
FILE REFERENCE: 34587-G-PCT-UBA
CURRENT APPLICATION NUMBER: US/09/644,460
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US99/04323
PRIOR FILING DATE: 1999-02-26

Sequence 26, Application US/09644460 Patent No. 6657053 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  637 CTATTATTTTTCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 GGGATGGGAATGTTTGTTCATAATAATTAGACATTTTCTATAGATATTTGACATTCTGC 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GGGATGGGAATGTTTGTTCATAAATAATTAGACATTTTCTATAGATATTTTGACATTCTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      757 GAAAGCAACAAACTGAAGACCAACTCCTATGAGAATATTATGAGATGTTTATGTAAT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           uery Match 22.3%; Score 186; DB 4; Length 219;
est Local Similarity 99.5%; Pred. No. 1.3e-39;
atches 197; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENERAL INFORMATION:
PAPLICANT: ENDEGE, WILSON O., BT AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
                                     equence 1995, Application US/09621976
atent No. 6639063
BNERAL INCORATION
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GRNSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PILING DATE: 2000-07-21
SOFTWARE: Patent.pm
EQ ID NO. 1956
LENGTH: 219
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CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/326,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASESEQ for Windows Version 3.0
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Sequence 376, Application US/09385982
Patent No. 6262334
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LCCATION: (1)...(611)
CTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
09-621-976-17956
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ORGANISM: Homo sapiens
ULT 3
09-621-976-17956
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LENGTH: 611
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20.4%; Score 170.2; DB 3; Length 611;

Query Match

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GENERAL INFORMATION:

APPLICANT: OLEK, Alexander
APPLICANT: DIEEK, Alexander
APPLICANT: DIEFENBROCK, Christian
APPLICANT: BEFLIAN, Ed.
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE OF INVENTION WIMBER: US/10/204,708
CURRENT APPLICATION WIMBER: DE 10019058.8
PRIOR APPLICATION WIMBER: DE 10019058.8
PRIOR APPLICATION WIMBER: DE 10019173.8
PRIOR APPLICATION WIMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION WIMBER: DE 10043826.1
PRIOR APPLICATION WIMBER: DE 10043826.1
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 8
SEQ ID NO 8
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                                                                                                     521 AACATACTTAATGTATTTTTATAGAACTTTGTAAACGAAAAGGAGATTCATGTTTTAGAAG 580
                                                                                                                                                                                                                                                                                        368 AACATACTTAATGGATTTTTATAGAACTTTGNAAACCAAAGGAGATTCATGTTTTANAAG 427
                                                                                                                                                                                                                                                                                                                                                                        428 rcriscicritritataricriscaadaaaar-rarginiscaggcintaaaraaarcccar 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 TGATGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCA 471
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                                                                                                                                                                       308 ANGTNCNGCCATTTTTNGTTTCNGGTAAACNGGAATATAANGNGAAAGAACAAACNTTGG 367
                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-8
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Best Local Similarity 51.1%; Pred. No. 0.0022;
Matches 143; Conservative 0; Mismatches 135; Indels
Best Local Similarity 78.2%; Pred. No. 2.8e-35;
Matches 204; Conservative 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          701 TGGGAATGTTTGTTCATAAAT 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10204708; Patent No. 6677731; GENERAL INFORMATION:
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US-10-204-708-8
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SOFTWARE: Fe
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730 ATTITCTATAGATATITGACATICTGCGAAAGCAACAAGCAAACTGAAGACCAACTCCTA 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTGTTTTCTTAAACCATTCTTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.4%; Score 45.2; DB 2; Length 177; Best Local Similarity 60.5%; Pred. No. 0.0096; Matches 92; Conservative 0; Mismatches 58; Indels 2
                                                                                                                                                                                          Sequence 20, Application US/09032684
Patent No. 5882874
GENERAL INFORMATION
APPLICANT: Fisher, Faul B.
TITLE OF INVENTION: DISPLAY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: COOPER & Dunham LLP
STREET: 1858 Avenue of the Americas
                                                                                                  1953 ATATÁTAĆGGGÍTÁTTTTTÍTTAÁTTTGATGTGATGTTTAG 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09644460
Sequence 20, Application US/09644460
Batent No. 6657053
GENERAL INFORMATION:
APPLICANT: Fisher, Faul B.
TITLE OF INVENTION: Reciprocal Subtraction Differential
                                                             650 CAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTG 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 recadadratraterrateratedadada 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55551/JPW/AMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 55551
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 391-055
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESULT 7
IS-09-644-460-20
                                                                                                                                                                                    -09-032-684-20
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-09-032-684-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        മ
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61 Grer--ergecacaerrigaeacrecegreaaagreagaageaacraaagaecaaergege 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 ATGTGGTTTACATATCTTTATGTACTGCCATTTTTTTGTTTCTGGTAAACTGGAATATAAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTAGGCAATAAAATGTTTTCAGAGGTGCGAAAAAGCTTTTTGTTTTTTTAAACCATTCTTA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.4%; Score 45.2; DB 4; Length 177; Best Local Similarity 60.5%; Pred. No. 0.0096; Matches 92; Conservative 0; Mismatches 58; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%; Score 45.2; DB 4; Length 832;
24.8%; Pred. No. 0.018;
tive 88; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: SSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION WIMBER: US/09/621,976
CURRENT APPLICATION WIMBER: US/09/621,976
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 2813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 790 TGAGAAATATTATGATGTTTATGTAAAGA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 regadadrirargrirargradadadada 150
TITLE OF INVENTION: Display
FILE REFERENCE: 34587-C-PCT-UGA
CURRENT APPLICATION NUMBER: UG/09/644,460
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US99/04323
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: US 09/197,889
PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: US 09/185,115
PRIOR APPLICATION NUMBER: US 09/185,115
PRIOR APPLICATION NUMBER: US 09/185,115
PRIOR APPLICATION NUMBER: US 09/185,115
PRIOR PILING DATE: 1998-11-03
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: RESUSED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-621-976-2813

Sequence 2813, Application US/09621976

Person No. 6639063

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
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Best local Similarity 24.0..
Rest local Similarity 24.0..
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..399
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; LOCATION: 235...
US-09-621-976-2813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             618654 AAATAATTTACAATAGGATCAAAATATTATGTTACACAATTTATTATTAAATGCCAATCA 618595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618831 TAATTTACATATTCTTTTATTGTAAGATTTGAAATTTTAAATATATTTCATGTTTTCTAT 618772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 TTTTTTGTTTCTGGTAAACTGGAATATAAAGTGAAAGAACAACATTGAACATACTTAA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               532 TGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGTCTGTCCTTTT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  502 GIGABAGAACAATITGAACATRACITAATGTATTTTTATAGAACTTTGTAAACGAAAG 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 TGATGTTGACATTATATTACTGCAAGATTAATGTGTGTTTACATATCTTTATGTACTGCCA 471
                                                                                                                        352 RWWAMWAWRRACAAATATATTATTTATGGTACAATTCTTGTACTTTAGCAAATCTGG 411
                                                                                                                                                                              412 AGTTAGTTCATAGTCAAGTCAGTTAATATTTCTTAGAGGAAAGTTTTGCTTTTTGTG 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuery Match 5.4%; Score 44.8; DB 4; Length 640681; set Local Similarity 52.1%; Pred. No. 0.34; latches 125; Conservative 0; Mismatches 112; Indels 3; Gaps
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504731-722-4
Sequence 4, Application US/08731722
Patent No. 5561971
GENERAL INFORMATION:
APPLICANT: Martin, Frank N.
TITLE OF INVENTION: Biocontrol of Fungal Soilborne Pathogens
TITLE OF INVENTION: by Pythium oligandrum
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANAIE, MASAHIRA
APPLICANT: SAKAKI, VASAHIRA
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 0813s6/01s9
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT APPLICATION NUMBER: US/09/790,988
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR PILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
<u>-</u>
                                                                                                                                                                                                                                                                                                                                                  equence 1, Application US/09790988 atent No. 6632935 ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Buchnera sp.
09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32606-6669
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09-790-988-1/c
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Sequence 4.2, Application US/10204708
Patent No. 667731
GENERAL INFORMATION:
APPLICANT: PIEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-606
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PLANDED DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 TAAACTGGAATATAAAGTGAAAGAACAAACATTTGAACATACTTAATGTATTTTTATAGA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 TAACTITTAAAAAAAATTAAAATGAAAATACTICTAATAAGAATATATTATTATAAAA 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 TATTAATTATTTAAATTGTGTAAATCCACCAGAAATTTTAACTATTATAAATATTG-AAG 558
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                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/731,722
                                                                                                                                                                                             TLILON LALLS

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: WILLIOCK, TEM 36,965.
REGISTRATION NUMBER: 36,965.
REFERENCE/DOCKET NUMBER: UF-16
TELEPHONE: 352-375-8100
INFORMATION 1908. 250 100: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: 17-1
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MEDIUM TYPE:
                                                                                                                                                                                FILING DATE:
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US-10-204-708-42
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7477 AGTITICAGIAGTITITITITITITITITIAAATAATITITITIAGAATITIGGAAATAAGG 7536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          517 TTTGAACATACTTAATGTATTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    637 CTATTATTTTTCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGGCA 696
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                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SECUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPECE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                 FEATURE:
OTHER HEFORMATION: chemically treated genomic DNA (Homo sapiens)
3-10-204-708-42
                                                                                                                                                                                                                                                                                                                                                           Query Match 5.2%; Score 43.8; DB 4; Length 8537; Best Local Similarity 51.0%; Pred. No. 0.11; Matches 128; Conservative 0; Mismatches 122; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STAILS.
COUNTRY: USA
ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows
SOFTWARE: FastSEQ for Windows
CUBRETT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
SEQ ID NOS: 98
LENGTH: 8537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 77, Application US/09221017B Patent No. 6444799 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICK APPLICATION DATA:
APPLICATION WUMBER: PP1182
FILING DATE: 3.DEC-1997
PRIOR APPLICATION DATA:
APPLICATION WUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7597 TAATTGAAAA 7607
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APPLICANT: Dobres, Michael S. and Mandaci, Sevnur TITLE OF INVENTION: A Plant Promoter Useful for Directing the TITLE OF INVENTION: Expression of Foreign Proteins to the Plant Epidermis NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5646333ris
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 ACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTGT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 TICIGGIAAACIGGAAIAIAAAGIGAAAGAACAAACAIIIGAACAIACIIAAIGIATIII 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 tiataagaaakagaargataatgagarritakcgccagtidraratgargaargifgt 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 TATAGAACTITIGIAAACGAAAGGAGAITCAIGITITIAGAAGICIGICCTITITIAIAICI 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 recarracitracaaaaaraaacecricarcacaeaacaarcarcarcarcricitraca 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 ACTITIATATIGATGCCATGTCAAGTGTTTTTCATACATAACTGTACAACAGGGTGATGA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 51.3%; Score 43; DB 4; Length 1189; Similarity 51.3%; Pred. No. 0.078; Observative 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: THIS CONTINUED TO THE STATE: PA COMPUTER READABLE FORM:
NEDIUM TYPE: FLOUDY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PTLING DATE: Herewith CLASSIFICATION: 435
                                                                                                         REGISTRATION NUMBER: 32,430
REFERENCE FOCKET NUMBER: 27340-20021.00
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELERAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 1199 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
ANTI-SENSB: UNKNOWN
ORIGINAL SOURCE:
ORIGINAL: PORYPHYROMONAS GINGIVALIS
ORGANISM: PORYPHYROMONAS GINGIVALIS
APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08299953
Patent No. 5646333
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 TGAAAGAAATCTAT 614
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NAME: Beardell, Lori Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: 1...1189
                                                                                     NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
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MOLECULE TYPE: DN
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US-09-221-017B-77
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Sequence 1, Application US/08459415
Sequence 1, Application US/08459415
Sequence 1, Application US/08459415
Patent No. 5744334
GENERAL INFORMATION:
APPLICANT DODIES, Michael S. and Mandaci, Sevnur
ATTLE OF INVENTION: Expression of Foreign for Directing the
TITLE OF INVENTION: Expression of Foreign Proteins to the Plant Epidermis
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS;
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5744334ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 GTACTGCCATTTTTGTTTCTGGTAAACTGGAATATAAAGTGAAAGAACAATTTGAA 522
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STATE: PA
STATE: PA
STATE: 19103
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: IBM PC COMPACIBLE
COMPUTER: PACENTIAN PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,415
TT:TNG DATE: 02-UN-1995
REGISTRATION NUMBER: 34,293
REPERNCE/DOCKT NUMBER: NOVA-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-564-8960
INFORMATION 5-564-8960
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2861 base pairs
TYPE: nucleic acid
STRANDENESS: double
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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08-299-953-1
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APPLICANT: Dobres, Michael S. and Mandaci, Sevnur TITLE OF INVENTION: A Plant Promoter Useful for Directing the TITLE OF INVENTION: Expression of Foreign Proteins to the Plant Epidermis UNMER OF SEQUENCES.

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     403 TGTTCATGATGATGTTGACATTATATTACTGCAAGATTAATGTGGTTTACATATCTTTAT 462
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5.1%; Score 42.8; DB 1; Length 2861;
Best Local Similarity 48.7%; Pred. No. 0.13;
Matches 113; Conservative 1; Mismatches 118; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6339185ris
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 TGTCCTTTTTATATCTTGAAAGAAATCTATGTATGATGCTATAAAATAAA 634
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVA-0003
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTATION UNDERF: 34,293
REFERENCE/DOCKET AUMBER: NOVA-
TELECOMMUNICATION INFORMATION:
TELEFAN: 215-564-8960
TELEFAX: 215-564-8960
TELEFAX: 215-568-3439
INFORMATION FOR SEC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2861 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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; Sequence 1, Application US/09066687
; Patent No. 6339185
                                                                                                      MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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LENGTH: 2861 base pairs
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                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                          linear
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                                                                                          TOPOLOGY:
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sarch completed: March 17, 2004, 14:25:20
b time : 95 secs

10 US-09-871-161-376
9 US-09-988-842A-355
11 US-09-938-842A-355
11 US-09-938-842A-355
12 US-09-938-842A-355
13 US-09-9770-961-618
14 US-10-94-0938-2020
15 US-09-108-975-2102
16 US-09-108-975-2102
17 US-10-11-455-2102
18 US-10-311-455-2102
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13.1 486 13.1 486 13.1 4986 11.8 533 10.9 718 8.6 60 1 6.5 3673778 6.3 113515 14

1170.2 1109.4 109.4 98.6 91

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Sequence 1113, Sequence 104, 3

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Sequence 545, App Sequence 939, App Sequence 939, App Sequence 939, App Sequence 56189, A Sequence 56189, A Sequence 2101, App Sequence 2101, App Sequence 2101, App Sequence 2101, App Sequence 2101, App Sequence 2101, App Sequence 2105, App Sequence 318, App Sequence 318, App Sequence 318, App
                                                                                                                                                      March 17, 2004, 12:27:16; Search time 379 Seconds (without alignments) 8111.172 Million cell updates/sec
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1 ggcacgaggcttgagcgcag......taaagacatgtaactgtctt 835
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-921-300-339
US-10-033-528-939
US-10-099-926-939
US-10-085-785A-56189
US-10-085-785A-56189
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US-10-245-535A-21733
US-10-245-525-2101
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US-10-245-525-2101
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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                                                                                                                                                                   APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERBNCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO/05988
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEO ID NOS: 1890
SEQ ID NOS: 1890
SEQ ID NO 545
LENGTH: 778
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature (552) OTHER INFORMATION: n equals a,t,g, or c
                                                                                                       Sequence 545, Application US/09925300 Patent No. US20020151681A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Best Local S
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                                                                         GATGATGTTGACATTATATTACTGCAAGATTAAATGTGGTTTTACATATCTTAATGTACTGC
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; Sequence 939, Application US/10033528
; Publication No. US20020131971A1
; GRNERAL INFORMATION:
   APPLICANT: King Gordon E.
   APPLICANT: King Gordon E.
   APPLICANT: Weagher, Madeleine Joy
   APPLICANT: Weagher, Madeleine Joy
   APPLICANT: Weagher, Madeleine Joy
   APPLICANT: Neagher, Jangchunt
   APPLICANT: Weagher, Jangchunt
   APPLICANT: Secrist, Heather
   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
   TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
   FILE REFERENCE: 210121:547C1
   CURRENT APPLICATION NUMBER: US/10/033,528
   NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSEQ for Windows Version 4.0
; FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD: FEWARD:
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CONGANISM: Homo sapiens
US-10-033-528-939
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US-10-033-528-939/c
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86 CACTICCTTCCTTCGCCTCACCCTCCCCAGTGCACTGAAGAAGGTAACCGGGTCCAGACC 145
                                              75 CACTICCTICCTICCTCCCCCACCCCCCAGTGCACTGAAGGTAACCGGGTCCAGACC 134
                                                                                                                                                                                                             386 GAGCTGCTTCTGCAAGGTGTTCATGATGTTGACATTATATTACTGCAAGATTAATGT 445
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                                                                                                                                           255 GGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATGAATGTGCCAACCTCTTT
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APPLICANT: Magagher, Madeleine Joy
APPLICANT: Magagher, Madeleine Joy
APPLICANT: Xu, Jiangchur
APPLICANT: Xu, Jiangchur
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REPERENCE: 210121.547
CURRENT FILING DATE: 2001.07-31
NUMBER OF SEQ ID NOS: 1789
SEQ ID NO 939
SEQ ID NO 939
LENGTH: 552
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Pred. No. 5.7e-123;
0; Mismatches 2; Indels 0;
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Sequence 939, Application US/09920300A
Patent No. US20020136728A1
GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 544; Conservative
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US-09-920-300A-939
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Query Match
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US-10-085-783A-56189
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             CATITITITIGATITICIGGIAAACTGGAATATAAAGTGAAAGAACAAACATTTGAACATACTT 529
                                                                               372 CATITITIGENERA PARCEGGA A TATA A A GEGA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA A GARA 
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Sublication No. US20030166064A1
SUBLICANT: WorkerTON:
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Xo. Jiango, Uninghun
APPLICANT: Xo. Jiango, Yuqiuu
APPLICANT: Xo. Jiango, Yuqiuu
APPLICANT: Jiang, Yuqiuu
APPLICANT: Jiang, Yuqiuu
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Sequence 56189, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: Clondcodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REPRENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/205,340
PRIOR FILING DATE: 2001-07-13
PRIOR PRILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR PRILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFFWARE: Patentin Version 3.2
LENGTH: 483
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TYPE: DNA
ORGANISM: Homo sapiens
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427 ATTACTGCAAGATTAATGTGGTTTACATATCTTTATGTACTGCCATTTTTTGTTTCTGGT 486
                                         311 ATTACTGCAAGATTAATGTGGTTTTACATATCTTTATGTACTGCCATTTTTTGTTTCTGGT 370
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TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT PILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR PILING DATE: 2002-06-28
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 56189, Application US/10242535A
Ublication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: Chondrodene Inc.
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SOFTWARE: Patentin version 3.2
SEQ ID NO 56189
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                                                                                                                                                                                                                                                                                                                             SULT 6
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S-10-242-535A-56189
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 AAATCCTATTATTTTTCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCG
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431 CTITGTAAACGAAAGGAGATTCATGTTTTAGAAGTCTGTCCTTTTTTTATATCT 483
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US-09-880-107-687
                                                                                                                                                                                                                                                                                                                                                                                                         STATEMENT IN TRUCKLIATION:

APPLICANT: HOTHE, Darci T.

APPLICANT: Ockley, Joseph G.

APPLICANT: Ockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

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TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles

TITLE OF OFFICE AND TOWNER: US 60/231,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR ENTING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR PRIOR PRIOR OFFICE AND TOWNER: US 60/237,054

PRIOR PRIOR FILING DATE: 2000-06-14

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PRIOR PRIOR OFFICE AND TOWNER: US 60/237,054
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; Sequence 687, Application US/09880107
Patent No. US20020142981A1
; GENERAL INFORMATION:
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APPLICANT: Chondrogene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REPERENCE: 4231/2005
FULE REPERENCE: 4231/2005
FULE REPERENCE: 231/2005
FULE REPERENCE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/095,783
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CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR PAPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PILING DATE: 2001-03-12
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PAECHLIN VETBÍON 3.2
IEUGTH: 400
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LOCATION: (23)...(23)
OTHER INFORMATION: n is a, c, g, or t
FRATURE:
NAME/KEY: misc_feature
LOCATION: (48)..(48)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (328). (328)
CHER INFORMATION: n is a, c, g, or t
-10-085-783A-21733
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3-10-242-535A-21733
                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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181 GCGCAGAGAGCAGCAATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAATTCA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TGATGATAAATGTGCCAACCTCTTTGAAGCATTGGTAGGAACTCTTAAAGCTGCAAAACG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 CATTATATTACTGCAAGATTAATGTGGTTTTACATATCTTTATGTACTGCCATTTTTTGTT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGAAGAAGTAACCGGGTCCATTNTCCACGCGCCGCCAGTTCTCCGGCNGGAAGGAAACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 AAGGAAGATIGIAACATAICCAGGAGAGCIGCTICTGCAAGGIGTTCATGATGTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 96.8%; Pred. No. 2.4e-83;
Matches 387; Conservative 0; Mismatches 13; Indels
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Patent No. US2002017552A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
FILE REPERENCE: 210121.527
CURRENT APPLICANTION NUMBER: US/09/878,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 TCTGGTAAACTGGAATATAAAGTGAAAGAACAAACATTTG 520
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PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR PLING DATE: 2001-03-12
PRIOR PRIOR PAPLICATION NUMBER: US 60/271,955
PRIOR PRIOR DATE: 2001-03-28
NUMBER OF SEC ID NOS: 58994
SCOFTWARE PACENTIN Version 3.2
LENGTH: 400
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: (23)__.(23)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (48)__.(48)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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LOCATION: (328)
, OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-21733
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                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
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525 TACTTAATGTATTTTTATAGAACTTTGTAAACGAAAGGAGATTCATGTTTTAGAAGTCTG 584
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Publication No. US20020156011A1
APPLICANT: Jiang, Vigiu
APPLICANT: Jiang, Vigiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Jiun A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND SIGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NONDER: US/10/046,935
CURRENT FILICATION DIAGNER: US/10/046,935
CURRENT FILICATION NOS: 2239
SOFTMARE: FASESQ for Windows Version 4.0
SEQ ID NO 2101
LENGTH: 365
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                                                                                                                                                                                                                                                                                                                                                    Query Match 43.6%; Score 364; DB 9; Length 365; Best Local Similarity 99.7%; Pred. No. 3.3e-79; Matches 364; Conservative 0; Mismatches 1; Indels
NUMBER OF SEQ ID NOS: 2237
SOSTWARE FRALSEQ for Windows Version 4.0
SEQ ID NO 2101
LENGTH: 365
                                                                                                                                                                                                                                         LOCATION: (1)...(365)
OTHER INFORMATION: n = A,T,C or G-09-878-178-2101
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: LOCATION: 273

- OTHER INFORMATION: n = A,T,C or G

:: US-10-046-935-2101
                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (1)...(365)
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                                                                                                                           TYPE: DNA
ORGANISM: Homo sapien
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365 ACTGCCATTTTTTGTTTCTGGTAAACTGGAATATAAAGTGAAAGACAACATTTGAACA 306
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                                                                                                                                                                                                                                        305 TACTTAATGTATTTTTATAGAACTTTGTAAACNAAAGGAGATTCATGTTTTAGAAGTCTG 246
                                                                                                                                                                                                                                                                                         585 ICCITITITADATCITGAAAATCIAIGIAIGIAIGCIAIAAAIAAAIAAAICCIAIIAIT 644
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                             0; Gaps
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APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121:527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FRASESQ for Windows Version 4.0
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99.7%; Pred. No. 3.3e-79;
live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2101, Application US/10146502 Publication No. US20030069180A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: n = A,T,C or G
US-10-146-502-2101
                             364; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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OCATION:
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645 ȚITCTCAGGAAICTGGITAGGAAIIGCAGGCAAIGAGAITTITIGCGGGGGAGGAIGGG 704
                                                                                      185 TITCTCAGGAATCTGGTTAGGAATTGCAGGCAATGAGATTTTTTGCGGGCAGGGATGGG 126
                                                                                                                                                                   705 AAIGITIGITCAIAAAIAAITAGACAITITCIAIAGATAITIGACAITCIGCGAAAGCAA 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 GGTTCAAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGAT 307
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                                                                                                                                                                                                                                 125 AATGTTTGTTCATAAATAATTAGACATTTTCTÄTÄGATATTTGACATTCTGCGAAAGCAA 66
                                                                                                                                                                                                                                                                                                                                    65 CAACCAAACTGAAGACCAACTCCTATGAGAAATATTATGATGTTTATGTAATAAAGACAT 6
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Sequence 26075, Application US/09918995
Publication No. US2030073623A1
SEMERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPRENCE: 20411-756
CURRENT APPLICATION WINBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/218,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SSOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO SCOTS
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Patent No. US20020055627A1
Patent No. US20020055627A1
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
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LOCATION: (1)...(458)
OTHER INFORMATION: n = A,T,C or G
3-09-918-995-26075
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S-09-925-299-318
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
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LOCATION: (227)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or NAME/GY: misc feature
LOCATION: (1987)
OTHER INFORMATION: n equals a,t,g, or
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KEY: misc feature
TION: (144)
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KEY: misc_feature
TION: (159)
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THER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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LOCATION: (150)
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OTHER INFORMATION: n equals a,t,g, or
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INFORMATION: n equals a,t,g, or
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INFORMATION: n equals a,t,g, or
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INFORMATION: n equals a,t,g, or
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OTHER INPORMATION: n equals a,t,g,
NAME/KEY: nisc_feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g,
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FION: (146)
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LOCATION: (196)
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ORGANISM: Homo sapiens
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Page

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134 CGGGTCCAGACCCACGCGCGCGCAGTTCTCCGGCGCAAGAAAACCGCGCACAAGAA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 GCAATGAATGIGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 NTAATGAATGTGGATCACGAGGATANCCNNTTAGTGNAGGAANTNCATCGTTTGGGTNTA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 AAAAATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAATGT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AAAAATGCTGATGGAAAGTTAANTGTGAAATTGGGGTCCTCTTTCGTGATGATAANTGA 317
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22.6%; Score 188.4; DB 9; Length 388;
Best Local Similarity 82.8%; Pred. No. 4.2e-36;
Matches 198; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
TITLE REFERENCE: PAID.

URRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                            LOCATION: (255)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (280)
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NAME/KEY: misc feature
LOCATION: (355)... - ....... a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
T.OCATION: (368)
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                                           OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature LOCATION: (240)
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NAME/KEY: misc feature
LOCATION: (242)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (314)
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NAME/KEY: misc_feature
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S-09-925-299-318
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Publication No. US20030040617A9
GENERAL INFORMATION:
NAME/KEY: misc feature
LOCATION: (234)
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ORGANISM: Homo sapiens
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JS-09-925-299-318
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LENGTH: 388
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OCATION: (196)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (222)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (154)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (160)
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LOCATION: (163)
NAME, KEY: misc feature
LOCATION: (168)
O'THER INFORMATION: n equals a,t,g, or c
NAME, KEY: misc feature
LOCATION: (168)
O'THER INFORMATION: n equals a,t,g, or c
LOCATION: (171)
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (143)
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NAME/KEY: misc feature
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LOCATION: (1)
OTHER INFORMATION: n equals a,t,g, or c
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
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LCCATION: (1146)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LCCATION: (150)
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LOCATION: (3180)
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NAME/KEY: misc_feature
LOCATION: (3180)
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LOCATION: (3170)
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LOCATION: (3170)
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LOCATION: (3170)
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NAME/KEY: misc_feature
LOCATION: (3170)
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NAME/KEY: misc_feature
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LOCATION: (3170)
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NAME/KEY: misc_feature
LOCATION: (3170)
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LOCATION: (3170)
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NAME/KEY: misc_feature
LOCATION: (3170)
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NAME/KEY: misc_feature
LOCATION: (3170)
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arch completed: March 17, 2004, 14:31:49 btime: 385 secs

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1 MAVDHEVNLLVEBIHRLGSK.....PGBLLLQGVHDDVDIILLQD
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                     protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ipt	BM752941 K EST0029 BU199007 DCBCT029 BU199007 DCBCT026 N39717 yx92d07.rl BG944512 ax56e07.x BX474507 DKFZ5666E BU198216 DCBCNC04 BB145690 ILC-HT020 CA33574 AV753954 AV753954 CB162901 K EST0223 AV714738 AV714738 AV716706 AV716706 BU58177 indcoll.y AV133406 HA2013 Hu BG563686 602584452 BG774708 ila4e02.y BG774405 602723144 BX110370 BX110370 BX110370 BX110370 BX110370 BX110370 BX110370 BX110370 BY715659 AV716659 BE89176 601434485 AV716653 AV716659 BE89176 601434485 AV716724 AV716363 BY716659 AV716659 BU59813 AGENCOURT BG58019 602579350 BU59813 AGENCOURT BG58019 AGENCOURT BG7800713 AGENCOURT BG780070 AGENCOURT BG780070 AGENCOURT BG78007772 BG780000RT BG78007772 BG780000RT BG78007777 BG80000RT BG7800777 BG80000RT BG7800777 BG80000RT BG7800777 BG80000RT BG7800777 BG80000RT BG7800777 BG80000RT BG7800777 BG80000RT BG7800777 BG8000RT BG7800777 BG80000RT BG7800777 BG80000RT BG7800777 BG8000RT BG7800777 BG8000RT BG7800777 BG8000RT BG7800777 BG8000RT BG7800777 BG8000RT BG780077 BG8000RT BG7800 BY777 BG8000RT BG7800 BY777 BG800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 BF800 B	
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LTION	K-EST0029681 S3SNU16 Homo Bapiens cDNA clone S3SNU16-30-F01 5',
	mRNA sequence.
CESSION	BM752941
RSION	BM752941.1 GI:19082559
YWORDS	BST.
URCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
	Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
FERENCE	1 (bases 1 to 477)

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DEFINITION
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SKim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,J.S., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and 21C Frontier Korean EST Project 2001

L Unpublished (2002)

Conteat: Kim YS

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52 Booun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 30 row: F column: 01

High quality sequence scop: 477.
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db_xref="taxon:9606"
clone="S3SNU16-30-F01"
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N39717 Soares melanocyte 2NbHM Homo sapiens cDNA_Clone IMAGE:269197 5', mRNA sequence.
        EST 05-SEP-2002
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1. (bases 1 to 480)

Xu, Xu, Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Lu, G., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z., and Han, Z.

Homo sapiens cDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                               Confact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 AIGAATGGGGTCACGAGGTTAACCTCTTAGTGGAAGAATTCATCGTTTGGGTTCAAAA
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/organism="Homo sapiens"
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Location/Qualifiers
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Pred. No.:
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/note="Organ: blood; Vector: Lambda ZAP II; Site 1: ECORI; Site 2: ECORI; 65,000 proliferating erythroid cells from Site 2: ECORI; 65,000 proliferating erythroid cells from the Duffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythroboietin. Total RNA was purified from the sorted cell population using TRIZOI reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapRinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested lambda Zap II vector (Stratagne). The phage library was amplified once prior to in vivo excision in Solk cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Logards Jeffery L. Miller
Laborators of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jm/f@nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 56 row: e column: 07
Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                           BG944932 SXT 15-JAN-2003 ax56e07.XI Hembase; Erythroid Progenitor Cells (LCB:ax library) Homo sapiens CDNA clone ax56e07 random, mRNA sequence.
270 TAICCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGATGATGATGATAATAATAATAACTGCAA 329
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(L. Dases I to 542)

(L. Dases I to 542)

(L. Dases I to 542)

(L. Dases I to 542)

(Gene expression in proliferating human erythroid cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev stage="Progenitor; BPO responsive CD71++++"
/lab_host="SOLR"
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Matches:
Conservative:
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/db_xref="taxon:9606"
/clone="ax56e07"
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Pred. No.:
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AUTHORS
TITLE
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COMMENT
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KEYWORDS
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BG944932
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Concact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Fat: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Figh quality sequence stops: 414
High quality sequence stops: 414
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAATTCATCGTTTGGGTTCAAAA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AsnalaaspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AsnieuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
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/organism="Homo sapiens"
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High quality sequence stop: 414.
Location/Qualifiers
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/db_xref="GDB:3878839"
/db_xref="taxon:9606"
/clone="IMAGE:269197"
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                                                                                                                                                                                                                                                                         The WashU-Merck EST Project
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N39717.1 GI:1163262
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                                                                           Homo sapiens (human)
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EST 05-SEP-2002
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                                                                                                                                                                                                                                                                         128 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATGATGTGCC 187
                                                                                                                                                                                    68 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 127
                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 567)

Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, Y., Qu, B., Gu, W., Tu, Y., Hons, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z., and Han, Z.

Homo sapiens CDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                             21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                    41 AsnLeuPheGluhlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                         61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zequang Han
Contact: Zequang Han
Contact: Zequang Han
Contact: Zequang Han
Contact: Zequang Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
20123, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-5080192.
Email: hanzg@chgc.81.cn.
Location/Qualifiers
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/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                       1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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DCBCNC04 DCB Homo sapiens CDNA, mRNA sequence.
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/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCB"
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/db_xref="taxon:9606"
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                                                                                              US-09-648-310-4 (1-81) x BX474507 (1-544)
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Best Local Similarity:
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VERSION
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JOURNAL
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BU198216
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DXFZp686E19170_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Choo, G., Han, M. and Wiemann, S.
EST (Bloecker, Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.) Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Sesarch Center (DKFZ); Brail s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biorechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                             192 Archargrecarcaccacerraaccrerracrecacaaarrecarcerrecaraa 251
                                                                                                                                                                                                                                                        252 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCCTTCCGTGATGATAAATGTGCC 311
                                                                                                                                                                                                                                                                                                                                                           312 AACCICITIGAAGCATIGGTAGGAACTCITAAAGCTGCAAAACGAAGGAAGATIGTAACA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                 372 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATTATATTACTGCAA 431
                                                                                                                                                                                                                                                                                                               41 AsnleuPheGlualaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
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                                                                                                                                                                                                                                                                                                                                                                                                      61 TyrProGlyGluLeuLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
                                                                                                                                    1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 544)

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/dev_etage="adult"
/lab_host="BH10B"
/clone lib="686 (synonym: hlcc3)"
/note="Vector: prriplEx2; Site_1: SfilA; Site_2: SfilB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No si sequence available.
This clone (DKPZp686E19170) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERRMANY; Email: clone@rzpd.de.
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                  Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases to 571)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, S.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=ILO-HT0205-131199-143-b09&t3=1999-11-13&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE145690 571 bp mRNA linear EST 21-JUN-2000 ILO-HT0205-131199-143-b09 HT0205 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                   201 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 260
                                                                                                                                                            261 AACGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGAAATGTGCC 320
                                                                                                                                                                                                                                                                  321 AACCICITIGAAGCATIGGIAGGAACICITAAAGCIGCAAAACGAAGGAAGAITGIAACA 380
                                                                                                                 40
1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys 20
                                                                                                                                                                                                                 41 AsnLeuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                      61 TyrProGlyGluLeuLeuClnGlnGlyValHisAspAspValAspIlelleLeuLeuGln 80
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                        21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspLysCysAla
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High quality sequence start: 26
High quality sequence stop: 571.
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0205"
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Sukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E. 1 (Dases 1 to 576)
NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L. Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Nobert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGCC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATTATATTACTGCAA 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
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/clone 11b="COGENE 4AR (4EAR)"
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.3-1.6 kb.
Normalized to Cot10, Primary library, non-amplified.
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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/dev stage="embryo, 4 weeks postconception"
/lab_host="DH108"
                                                                                                                           Conservative:
Mismatches:
Indels:
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                                          Length:
Matches:
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/clone="IMAGE:5606886"
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CA335746.1 GI:24553844
                                               .26e-45
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Best Local Similarity:
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Alignment Scores:
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/clone lib="TP"
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Best Local Similarity:
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1. (Dases 1 to 599)

Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Cao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Zhang, Q., Han, Z., Chen, Z. and Chen, J. Hang, C., Han, Z., Chen, Z. and Chen, J. Homo sapiens TP library cDNA clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV753954 BST 19-OCT-2000 AV753954 TP Homo sapiens cDNA clone TPAASB04 5', mRNA sequence.
Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
http://hg.wastl.edu/COGENE/."
                                                                                                                                                                                                                                                                                                                                   82 ATGAATCTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 141
                                                                                                                                                                                                                                                                                                                                                                                                              142 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATGAATGTGCC 201
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Ashanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64170045(ex.663332)
Fax: 86-21-64743206
Fmal: mbshi@mes.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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/dev_stage="Adult"
/lab_host="BM25,8"
                                                                                                                                                                                                         Indels:
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TPAASB04"
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CB162901 559 bp mRNA linear BST 30-JAN-2003
E.SET022398 LIBPOOLIN1 Homo sapiens CDNA clone LIBPOOLIN1-41-G10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Li8tPOCLIN1"
/note="Organ: Liver; Vector: pT7T3-Pac, Site_1: BcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TyrProGlyGluLeuLeuGlnGlyValHisAspAspValAspIleIleLeuLeuGln 80
                                                                                                                                                                                                                                                                                             21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AsnieuPheGluAlaLeuValGlyThrieuLysAlaAlaLysArgArgLysIleValThr 60
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
                                                                                                                                                                                                                                                                      1 MetAsnValAspHisGluvalAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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Korea Research Institute of Bioscience & Biotechnology
52 Bosun-dong Vaseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-4409
Fax: +82-42-866-4409
Email: yongsung@mail.kribb.re.kr
Plate: 41 row: G column: 10
Plate: 41 row: G column: 10
High quality sequence stops: 599.
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Matches:
Conservative:
Mismatches:
Indels:
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Xin, Y.S.
21C Frontier Korean EST Project 2001
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                                                                                  3.47e-45
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AV714738
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."
                                                                                                                                                                                                                                                                                                              146 ATGAATGTGGGATCACGAGGTTAACCTCTTAGTGGAGAAATTCATCGTTTGGGTTCAAAA 205
                                                                                                                                                                                                                                                                                                                                                                                   206 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAAATGTGCC 265
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Xu, Xu, Xu, Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,O., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Howo, Sapiens cDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                41 AsnieuPheGluAlaieuValGlyThrleuLysAlaAlaLysArgArgLysIleValThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="awx5.8"
/clone_lib="DCB"
/note="Vector: pTriplEx2; Site_l: sfilA; Site_2: sfilS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
2012 0.0 Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
2012 0.0 Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
12012 0.0 Shouling Road, Park, Pudong, Shanghai
Tel: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                              1 MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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|db_xref="taxon:9606"
|clone="DCBBRC03"
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Homo sapiens
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st Local Similarity:
ery Match:
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                                                                                           ignment Scores:
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AUTHORS
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AV716706 AV716706 601 bp mRNA linear BST 16-OCT-2000 AV716706 DCB Homo sapiens cDNA clone DCBCFB05 5', mRNA sequence. AV716706
                                                                                                                                                                                                                                                           96 ATGAATGTGGATCACGAGGTTAACCTCTTAGTGGAGGAAATTCATCGTTTGGGTTCAAAA 155
                                                                                                                                                                                                                                                                                                                                                156 AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATGATGTGCC 215
                                                                                                                                                                                                                                                                                                                                                                                                                       276 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGTTGACATTATTATTACTGCAA 335
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                                                                                                                                                                                                                                                                                                        21 AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla 40
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I (basea I to 601)

Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Homo sapiens cDNA, DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Fax: 86-21-50801922
Fax: 86-21-50801922
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="DCB"
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                                                             Conservative:
Mismatches:
Indels:
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/mol type="makNa"
/db xref="raxon:9606"
/clone="DCBCFB05"
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/dev stage="mature"
/lab_nost="BM25.8"
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                                                           Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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Pred. No.:
Score:
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DB:
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AV716706
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/organism="Homo sapiens"
mol_type="mRNA"
db_xref="taxon:9606"
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/dev_stage="fetal"
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                                                                                                                                                                                                                                                                                                                                                US-09-648-310-4 (1-81) x BUS81717 (1-604)
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Ali33406.1 GI:6360722
EST.
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410.00
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Homo sapiens
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Best Local Similarity:
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I (bases I to 604)

I (bases I to 604)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wyle, T., Marrin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Jackson, Y. and Bowers, Y. Cole, R., Teagareishvili, R., Millans, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTS: in40c11.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, M. 1612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BUS81717 10.41 Human Fetal Pancreas 1B Homo sapiens CDNA 5' similar to TR:081881 081881 HYPOTHETICAL 18.3 KD PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                             373 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGATGTTGACATTATTACTGCAA 432
                                                                                                                                                         AATGCTGATGGAAAGTTAAGCGTGAAATTTGGGGTCCTCTTCCGTGATGATAATGTGCC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 617-495-1812
Tel: 617-495-1812
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Mashington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@imgate.wustl.edu)
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                                                                                                                                    20
                                                                                                                                                                                                                                                                                          AsnleuPheGluAlaLeuValGlyThrLeuLysAlaAlaLysArgArgLysIleValThr 60
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| organism="Homo sapiens"
| organism="Homo sapiens"
| mol_type="mRNA"
| db xref="texon:9606"
| tissue type="Fetal Pancreas (4 Pooled Donors, 18 - 20 weeks, Stratagene #738023)"
| dev_stage="Fetal Pancreas" | clone lib="Human Fetal Pancreas 18"
| clone lib="Human Fetal Pancreas 18"
| note="Vector: pBluescript SK(-); Site_1: NotI; Site_2:
                                                                                                                                                                                                               AsnAlaAspGlyLysLeuSerValLysPheGlyValLeuPheArgAspAspLysCysAla
                                                                                                                                    MetAsnValAspHisGluValAsnLeuLeuValGluGluIleHisArgLeuGlySerLys
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    Conservative:
Mismatches:
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High quality sequence stop: 450.
Location/Qualifiers
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Homo sapiens
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est Local Similarity:
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AI133406 634 bp mRNA linear EST 11-NOV-1999
HA2013 Human fetal liver cDNA library Homo sapiens CDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 AACCICTITGAAGCATIGGIAGGAACICTIAAAGCIGCAAAACGAAGGAAGAITGIAACA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 TATCCAGGAGAGCTGCTTCTGCAAGGTGTTCATGATGTTGACATTATATTACTGCAA 284
XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Bucild Ave., St. Louis, MO Fax:314-747-2692."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 634)
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Department of Hematology
Beijing Institute of Radiation Medicine
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
Fax: 0086-10-68214653
Email: Yyt48@yahoo.com.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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Percent Similarity:
Best Local Similarity:
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/mol_type="mRNA"
/db_xref="text=0.9606"
/clone="IMAGE:4712125"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 76"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
Sii (ggccgcctcggcc); Site_2: Siil (ggccattatggcc); 5' and
3 adaptors were used in Cloning as follows: 5' adaptor
sequence: 5' -AATCTAGAGGCGGCGGAGAGG-GT(30)BN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG563686 641 bp mRNA linear EST 10-APR-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 641)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLCM1553 row: h column: 14
High quality sequence stop: 641.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Matches:
Conservative:
Mismatches:
Indels:
/note="Vector: pCDNA1"
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C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Falo Alto, CA). Note: this is a NIH_MGC Library."
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